GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:05:30 ; Search time 26 Seconds
(without alignments)
389.870 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1891	87.9	368	4	US-08-709-838-2	Sequence 2, Appli
2	1891	87.9	368	4	US-08-829-839-2	Sequence 2, Appli
3	640	29.8	374	3	US-08-982-493-6	Sequence 6, Appli
4	635	29.5	372	1	US-08-202-056-5	Sequence 5, Appli
5	635	29.5	372	1	US-08-076-093A-6	Sequence 6, Appli
6	635	29.5	372	1	US-08-701-265-6	Sequence 6, Appli
7	635	29.5	372	2	US-08-284-586-6	Sequence 6, Appli
8	635	29.5	372	2	US-08-805-478-6	Sequence 6, Appli
9	635	29.5	372	2	US-08-802-627A-6	Sequence 6, Appli
10	635	29.5	372	2	US-08-801-238-6	Sequence 6, Appli
11	635	29.5	372	2	US-08-801-228-6	Sequence 6, Appli
12	635	29.5	372	3	US-09-104-296-6	Sequence 6, Appli
13	635	29.5	372	3	US-08-982-493-8	Sequence 8, Appli
14	633	29.4	355	1	US-07-759-568-1	Sequence 1, Appli
15	633	29.4	355	1	US-08-450-393A-8	Sequence 8, Appli
16	633	29.4	355	2	US-08-390-000A-5	Sequence 5, Appli
17	633	29.4	355	4	US-08-446-669-8	Sequence 8, Appli
18	633	29.4	355	5	PCT-US95-00476-8	Sequence 8, Appli
19	633	29.4	360	1	US-08-202-056-7	Sequence 7, Appli
20	605.5	28.1	350	1	US-08-202-056-1	Sequence 1, Appli
21	605.5	28.1	350	1	US-08-076-093A-2	Sequence 2, Appli
22	605.5	28.1	350	1	US-08-450-393A-7	Sequence 7, Appli
23	605.5	28.1	350	1	US-08-410-453A-1	Sequence 1, Appli
24	605.5	28.1	350	1	US-08-701-265-2	Sequence 2, Appli
25	605.5	28.1	350	1	US-08-410-454A-1	Sequence 1, Appli
26	605.5	28.1	350	2	US-08-284-586-2	Sequence 2, Appli
27	605.5	28.1	350	2	US-08-410-456A-1	Sequence 1, Appli
28	605.5	28.1	350	2	US-08-805-478-2	Sequence 2, Appli
29	605.5	28.1	350	2	US-08-802-627A-2	Sequence 2, Appli
30	605.5	28.1	350	2	US-08-801-238-2	Sequence 2, Appli
31	605.5	28.1	350	2	US-08-801-228-2	Sequence 2, Appli
32	605.5	28.1	350	3	US-09-104-296-2	Sequence 2, Appli
33	605.5	28.1	350	4	US-08-446-669-7	Sequence 7, Appli
34	605.5	28.1	350	5	PCT-US95-00476-7	Sequence 7, Appli
35	589.5	27.4	410	1	US-08-153-848-7	Sequence 7, Appli
36	589.5	27.4	410	3	US-09-299-843A-7	Sequence 7, Appli
37	589.5	27.4	410	4	US-09-088-337B-7	Sequence 7, Appli
38	589.5	27.4	410	5	PCT-US93-11153-7	Sequence 7, Appli
39	586	27.2	358	1	US-08-153-848-19	Sequence 19, Appl
40	586	27.2	358	3	US-09-299-843A-19	Sequence 19, Appl
41	586	27.2	358	4	US-09-088-337B-19	Sequence 19, Appl
42	586	27.2	358	5	PCT-US93-11153-19	Sequence 19, Appl
43	586	27.2	378	1	US-08-153-848-15	Sequence 15, Appl
44	586	27.2	378	3	US-09-299-843A-15	Sequence 15, Appl
45	586	27.2	378	4	US-09-251-545-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-709-838-2
; Sequence 2, Application US/08709838
; Patent No. 6140064
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,838
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  368 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-709-838-2

  Query Match            87.9%;  Score 1891;  DB 4;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 2.3e-148;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
                 |||||
Db     364 SYSGL 368


RESULT 2
US-08-829-839-2
; Sequence 2, Application US/08829839
; Patent No. 6184358
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    APPLICANT:  Qin, Shixin
;    APPLICANT:  Mackay, Charles R.
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,839
;      FILING DATE:  31-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/709,838
;      FILING DATE:  10-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  368 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-829-839-2

  Query Match             87.9%;  Score 1891;  DB 4;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 2.3e-148;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
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Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
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Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 3
US-08-982-493-6
; Sequence 6, Application US/08982493
; Patent No. 6110695
;  GENERAL INFORMATION:
;    APPLICANT:  Gunn, Michael D
;    APPLICANT:  Williams, Lewis T
;    APPLICANT:  Cyster, Jason G
;    TITLE OF INVENTION:  Modulating B Lymphocyte Chemokine /
;    TITLE OF INVENTION:  Receptor Interactions
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  75 DENISE DRIVE
;      CITY:  HILLSBOROUGH
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/982,493
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UCSFT98-026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 343-4341
;      TELEFAX:  (650) 343-4342
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  374 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-982-493-6

  Query Match             29.8%;  Score 640;  DB 3;  Length 374;
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Best Local Similarity 40.9%; Pred. No. 2.5e-45;
Matches 143; Conservative 54; Mismatches 139; Indels 14; Gaps 6;

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Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
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Db      26 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
             |||:||| |||||| |||  ||    : :| || |: |||   ||  ||||  :||:
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLV 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
           |||: |||| ||||   |||     : :|| |:|    |||||: :|      |::: |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
             | ::      |      | |  : |||||:||| :|| ::  ||   |  :| :|:
Db     202 -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |   : | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT 369
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RESULT 4
US-08-202-056-5
; Sequence 5, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-202-056-5

Query Match 29.5%; Score 635; DB 1; Length 372;
Best Local Similarity 40.8%; Pred. No. 6.5e-45;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

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Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   | :| :| |   :  ||       :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
             |  :|   |  |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :|||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
             ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
             |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
             ||  ||||||:|| | ||||  :  || :|||     | : ' | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
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RESULT 5
US-08-076-093A-6
; Sequence 6, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids

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;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-076-093A-6

  Query Match             29.5%;  Score 635;  DB 1;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:|||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :|| :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 6
US-08-701-265-6
; Sequence 6, Application US/08701265
; Patent No. 5776457
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,265
;      FILING DATE:  22-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-701-265-6

  Query Match             29.5%;  Score 635;  DB 1;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:|||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :|| :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 7
US-08-284-586-6
; Sequence 6, Application US/08284586
; Patent No. 5840856
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,586
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
```

```
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-284-586-6

  Query Match             29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 8
US-08-805-478-6
; Sequence 6, Application US/08805478
; Patent No. 5874543
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,478
;      FILING DATE:  25-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-805-478-6

  Query Match             29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 9
US-08-802-627A-6
; Sequence 6, Application US/08802627A
; Patent No. 5892017
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,627A
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-802-627A-6

  Query Match             29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |  |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |   | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 10
US-08-801-238-6
; Sequence 6, Application US/08801238
; Patent No. 5919896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,238
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-801-238-6

  Query Match             29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |  |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |   | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 11
US-08-801-228-6
; Sequence 6, Application US/08801228
; Patent No. 5922541
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  METHODS FOR DETECTION AND AMPLIFICATION OF
;    TITLE OF INVENTION:  PF4A RECEPTOR NUCLEIC ACID
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,228
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-801-228-6

  Query Match             29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| | |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :|||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 12
US-09-104-296-6
; Sequence 6, Application US/09104296
; Patent No. 6087475
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/104,296
;      FILING DATE:  24-June-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/701265
;      FILING DATE:  22-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/664228
;      FILING DATE:  06-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-104-296-6

  Query Match             29.5%;  Score 635;  DB 3;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| | |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :|||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
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Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 13
US-08-982-493-8
; Sequence 8, Application US/08982493
; Patent No. 6110695
;  GENERAL INFORMATION:
;    APPLICANT:  Gunn, Michael D
;    APPLICANT:  Williams, Lewis T
;    APPLICANT:  Cyster, Jason G
;    TITLE OF INVENTION:  Modulating B Lymphocyte Chemokine /
;    TITLE OF INVENTION:  Receptor Interactions
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  75 DENISE DRIVE
;      CITY:  HILLSBOROUGH
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/982,493
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UCSFT98-026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 343-4341
;      TELEFAX:  (650) 343-4342
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  372 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-982-493-8

  Query Match             29.5%;  Score 635;  DB 3;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 6.5e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | ||||| :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 14
US-07-759-568-1
; Sequence 1, Application US/07759568
; Patent No. 5374506
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Philip M.
;    TITLE OF INVENTION:  Cloning of cDNA Encoding a Functional
;    TITLE OF INVENTION:  Human Interleukin-8 Receptor
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/759,568
;      FILING DATE:  19910913
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scott, Watson T.
;      REGISTRATION NUMBER:  26581
;      REFERENCE/DOCKET NUMBER:  WTS/5683/91535/WBH
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 cush
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-759-568-1

  Query Match             29.4%;  Score 633;  DB 1;  Length 355;
  Best Local Similarity   40.1%;  Pred. No. 9e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| |||  |  |:|  |
Db      16 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 74

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
           | || :||:||:|| |  ||||:||      |:||: ||||   |  :|||:| |||||
Db      75 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 134

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||         ||::||| || |||  :|    :
Db     135 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 184

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   :  :|       |  ||:|    ||::|||:| :||   |  |  :   :
Db     185 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 240

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db     241 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 300

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           | |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db     301 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 352


RESULT 15
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```
US-08-450-393A-8
; Sequence 8, Application US/08450393A
; Patent No. 5707815
;  GENERAL INFORMATION:
;    APPLICANT:  Charo, Israel
;    APPLICANT:  Coughlin, Shaun
;    TITLE OF INVENTION:  MAMMALIAN MONOCYTE CHEMOATTRACTANT
;    TITLE OF INVENTION:  PROTEIN RECEPTORS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306-2155
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,393A
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cserr, Luann
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  UCAL-237/02US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5165
;      TELEFAX:  415-8857-0663
;      TELEX:  380816CooleyPA
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-08-450-393A-8

  Query Match             29.4%;  Score 633;  DB 1;  Length 355;
  Best Local Similarity   40.1%;  Pred. No. 9e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| |||| | |:| |
Db      16 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 74

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
            | || :||:||:|| |  ||||:||      |:||: |||| | :|||:| |||||
Db      75 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 134

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||         ||::||| || |||  :|    :
Db     135 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 184

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   :  :|      |  ||:|    ||::|||:| :||   |  |  :   :
Db     185 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 240

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db     241 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 300

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           | |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db     301 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 352


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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:11:20 ; Search time 49 Seconds
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Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09101518_@CGN_1_1_13_@runat_29102002_091056_29932 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1897	88.2	1670	3	US-08-709-838-1	Sequence 1, Appli
2	1897	88.2	1670	4	US-08-829-839-1	Sequence 1, Appli
3	640	29.8	2517	3	US-08-982-493-5	Sequence 5, Appli
4	635	29.5	1510	1	US-07-759-568-4	Sequence 4, Appli
5	635	29.5	1679	1	US-08-202-056-6	Sequence 6, Appli
6	635	29.5	1679	1	US-08-076-093A-5	Sequence 5, Appli
7	635	29.5	1679	1	US-08-701-265-5	Sequence 5, Appli
8	635	29.5	1679	2	US-08-284-586-5	Sequence 5, Appli
9	635	29.5	1679	2	US-08-805-478-5	Sequence 5, Appli
10	635	29.5	1679	2	US-08-802-627A-5	Sequence 5, Appli
11	635	29.5	1679	2	US-08-801-238-5	Sequence 5, Appli
12	635	29.5	1679	2	US-08-801-228-5	Sequence 5, Appli
13	635	29.5	1679	3	US-09-104-296-5	Sequence 5, Appli
14	635	29.5	1679	5	PCT-US94-06380-3	Sequence 3, Appli
15	635	29.5	1748	1	US-08-202-056-8	Sequence 8, Appli
16	635	29.5	2818	3	US-08-982-493-7	Sequence 7, Appli
17	635	29.5	2818	4	US-08-628-655-1	Sequence 1, Appli
18	621.5	28.9	1200	5	PCT-US95-03032-1	Sequence 1, Appli
19	620	28.8	1106	5	PCT-US92-02977-5	Sequence 5, Appli
20	620	28.8	1106	5	PCT-US95-03032-4	Sequence 4, Appli
21	615	28.6	1373	5	PCT-US92-02977-6	Sequence 6, Appli
22	615	28.6	1373	5	PCT-US95-03032-3	Sequence 3, Appli
23	609	28.3	1176	5	PCT-US95-03032-2	Sequence 2, Appli
24	609	28.3	1933	1	US-08-076-093A-1	Sequence 1, Appli
25	609	28.3	1933	1	US-08-410-451-1	Sequence 1, Appli
26	609	28.3	1933	1	US-08-410-455-1	Sequence 1, Appli
27	609	28.3	1933	1	US-08-418-919-1	Sequence 1, Appli
28	609	28.3	1933	1	US-08-410-453A-2	Sequence 2, Appli
29	609	28.3	1933	1	US-08-701-265-1	Sequence 1, Appli
30	609	28.3	1933	1	US-08-410-454A-2	Sequence 2, Appli
31	609	28.3	1933	2	US-08-284-586-1	Sequence 1, Appli
32	609	28.3	1933	2	US-08-410-456A-2	Sequence 2, Appli
33	609	28.3	1933	2	US-08-805-478-1	Sequence 1, Appli
34	609	28.3	1933	2	US-08-802-627A-1	Sequence 1, Appli
35	609	28.3	1933	2	US-08-801-238-1	Sequence 1, Appli
36	609	28.3	1933	2	US-08-801-228-1	Sequence 1, Appli
37	609	28.3	1933	3	US-09-104-296-1	Sequence 1, Appli
38	609	28.3	1933	5	PCT-US94-06380-1	Sequence 1, Appli
39	607.5	28.2	1200	5	PCT-US92-02977-1	Sequence 1, Appli
40	605.5	28.1	1883	1	US-08-202-056-2	Sequence 2, Appli
41	589.5	27.4	1900	1	US-08-153-848-18	Sequence 18, Appl
42	589.5	27.4	1900	3	US-09-299-843A-18	Sequence 18, Appl
43	589.5	27.4	1900	4	US-09-088-337B-18	Sequence 18, Appl
44	589.5	27.4	1900	5	PCT-US93-11153-18	Sequence 18, Appl
45	589.5	27.4	2058	1	US-08-153-848-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-709-838-1
; Sequence 1, Application US/08709838
; Patent No. 6140064
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TKI96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs

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;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  69..1172
US-08-709-838-1

Alignment Scores:
Pred. No.:                3.18e-202       Length:         1670
Score:                    1897.00         Matches:        369
Percent Similarity:       97.63%          Conservative:   1
Best Local Similarity:    97.36%          Mismatches:     5
Query Match:              88.19%          Indels:         4
DB:                       3               Gaps:           1

US-09-101-518A-2 (1-415) x US-08-709-838-1 (1-1670)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||          ||||||          :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 2
US-08-829-839-1
; Sequence 1, Application US/08829839
; Patent No. 6184358
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    APPLICANT:  Qin, Shixin
;    APPLICANT:  Mackay, Charles R.
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,839
;      FILING DATE:  31-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/709,838
;      FILING DATE:  10-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  69..1172
US-08-829-839-1

Alignment Scores:
Pred. No.:                3.18e-202       Length:         1670
Score:                    1897.00         Matches:        369
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Percent Similarity:     97.63%          Conservative:  1
Best Local Similarity:  97.36%          Mismatches:    5
Query Match:            88.19%          Indels:        4
DB:                     4               Gaps:          1

US-09-101-518A-2 (1-415) x US-08-829-839-1 (1-1670)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||          ||||||           :::||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
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Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
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Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 3
US-08-982-493-5
; Sequence 5, Application US/08982493
; Patent No. 6110695
;  GENERAL INFORMATION:
;    APPLICANT:  Gunn, Michael D
;    APPLICANT:  Williams, Lewis T
;    APPLICANT:  Cyster, Jason G
;    TITLE OF INVENTION:  Modulating B Lymphocyte Chemokine /
;    TITLE OF INVENTION:  Receptor Interactions
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  75 DENISE DRIVE
;      CITY:  HILLSBOROUGH
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/982,493
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UCSFT98-026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 343-4341
;      TELEFAX:  (650) 343-4342
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2517 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1122
US-08-982-493-5

Alignment Scores:
Pred. No.:              1.76e-61        Length:         2517
Score:                  640.00          Matches:        143
Percent Similarity:     56.29%          Conservative:   54
Best Local Similarity:  40.86%          Mismatches:     139
Query Match:            29.75%          Indels:         14
DB:                     3               Gaps:           6

US-09-101-518A-2 (1-415) x US-08-982-493-5 (1-2517)

Qy      70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
           :::|||:::|||   :::           :::|||:::   |||   |||
Db      76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy      90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                          :::|||         |||:::|||      |||||||||
Db     127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186
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Qy    110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
          :::|||||||||||||:::::|||||      |||      :::|||         |||
Db    187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy    130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
          |||||||||:::|||||||||  ||||||||||||||||  ||||||
Db    247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy    150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
          |||      ||||||           :::   :::|||   ||||||   |||:::
Db    307 GTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy    170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
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Db    367 CTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTCGTG 426

Qy    190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
          |||||||||:::   ||||||||||||   ||||||||||||          |||||||||
Db    427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy    210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                :::   :::||||||   |||:::|||           ||||||
Db    487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy    230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
          |||||||||:::   :::|||                  |||:::::::::   |||
Db    547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

Qy    247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr------------AlaLeu 262
                |||   ::::::                  |||
Db    604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
          |||   |||      :::   ||||||||||||||:::|||||||||   :::||||||
Db    661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
                :::::      ||||||         |||      :::|||   :::|||:::
Db    721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy    302 ArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
          |||:::   ::::::|||         |||   |||||||||:::||||||||||:::|||
Db    781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840

Qy    322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
          :::   :::|||   |||   |||   |||:::      :::|||
Db    841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy    342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
             :::   ||||||   ::::::         ||||||      ||||||||||||||
Db    901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy    362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
          |||:::||||||   |||   ||||||||||||||      :::      ||||||
Db    961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy    382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
          :::||||||||||           |||      |||         :::   |||
Db   1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy    402 SerSerTrpSerGluThrSerGluAlaSer 411
          ||||||   ||||||:::      |||:::
Db   1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107

RESULT 4
US-07-759-568-4
; Sequence 4, Application US/07759568
; Patent No. 5374506
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Philip M.
;    TITLE OF INVENTION:  Cloning of cDNA Encoding a Functional
;    TITLE OF INVENTION:  Human Interleukin-8 Receptor
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cushman, Darby & Cushman
;      STREET:  1615 L Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/759,568
;      FILING DATE:  19910913
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scott, Watson T.
;      REGISTRATION NUMBER:  26581
;      REFERENCE/DOCKET NUMBER:  WTS/5683/91535/WBH
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 cush
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1510 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-759-568-4

Alignment Scores:
Pred. No.:              2.84e-61      Length:          1510
Score:                  635.00        Matches:         146
Percent Similarity:     53.56%        Conservative:    57
Best Local Similarity:  38.52%        Mismatches:      136
Query Match:            29.52%        Indels:          40
DB:                     1             Gaps:            8

US-09-101-518A-2 (1-415) x US-07-759-568-4 (1-1510)

Qy     50 SerGlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsn 69
          |||::::::   |||      :::   :::|||:::                  |||:::
Db     20 TCAAAAATGGAAGATTTTAACATGGAGAGTGACAGC--------------TTTGAAGAT 64

Qy     70 Phe--------------SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCys 84
          |||                |||:::|||   |||
Db     65 TTCTGGAAAGGTGAAGATCTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTA 124

Qy     85 CysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuPro 104
               :::   ||||||      :::   ||||||      ::::::   |||:::
Db    125 CTAGATGCCGCCCCATGTGAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTC 181

Qy    105 AlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaVal 124
             :::|||:::|||:::|||||||||   ||||||||||||      |||      |||
Db    182 ATTATCTATGCCCTGGTATTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTC 241

Qy    125 LeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaVal 144
          :::|||      |||         |||   ||||||   :::|||||:::||||||:::
Db    242 ATCTTATACAGCAGGGTCGGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTG 301

Qy    145 AlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrp 164
          ||||||   |||      ||||||||||||:::||||||                  |||
Db    302 GCCGACCTACTCTTTGCCCTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGG 361

Qy    165 ValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAla 184
          :::|||||:::   ||||||||||||         |||      :::|||||||||:::
Db    362 ATTTTTGGCACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGT 421

Qy    185 GlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr 204
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          |||   ||||||||||||||||||||   ||||||||||||   ||||||||||||||||
Db    422 GGCATCCTGCTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACA 481

Qy    205 GlnLeuTyrArgArgGlyProProAlaArgValThrLeuThr---------------- 218
          :::                              |||||||||
Db    482 CGC------------------------------ACACTGACCCAGAAGCGCTACTTGGTC 511

Qy    219 ---------CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
                  ||||||::::::|||||||||   ||||||   |||||||||      :::
Db    512 AAATTCATATGTCTCAGCATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTT 571

Qy    236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
          |||          :::        ::::::         |||         :::
Db    572 TTCCGAAGGACCGTCTACTCATCCAATGTTAGCCCAGCC---TGC---------TATGAG 619

Qy    256 GlnValGly-----------------ArgThrAlaLeuArgValLeuGlnLeuValAla 269
            :::|||                 |||      ||||||:::|||
Db    620 GACATGGGCAACAATACAGCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTT 679

Qy    270 GlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
          ||||||::::::|||||||||:::|||   :::||||||      |||      |||
Db    680 GGCTTCATCGTGCCACTGCTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTG 739

Qy    290 LeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValVal 309
              :::        ::::::   ||||||||||||:::::      ||||||:::
Db    740 TTTAAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTC 799

Qy    310 AlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAsp 329
            |||   |||||||||   ||||||:::||||||:::|||   |||   ||||||
Db    800 ATCTTCCTGCTTTGCTGGCTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGG 859

Qy    330 LeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
                :::        |||   |||   :::   :::|||   |||
Db    860 ACCCAGGTGATCCAGGAGACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCC 919

Qy    350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
          |||      ||||||   :::|||   |||||||||||||||:::|||||||||:::|||
Db    920 ACCGAGATTCTGGGCATCCTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGC 979

Qy    370 ValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArg 389
            |||||||||      :::      :::|||         |||      ::::::
Db    980 CAGAAGTTTCGCCATGGACTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGAC 1039

Qy    390 GlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
            |||   :::            |||        ||||||        ||||||
Db   1040 TCCCTGCCCAAAGACAGCAGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1096

RESULT 5
US-08-202-056-6
; Sequence 6, Application US/08202056
; Patent No. 5440021
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Lee, James
;    TITLE OF INVENTION:  Antibodies to Human IL-8 Type B Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,056
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-202-056-6

Alignment Scores:
Pred. No.:              3.36e-61      Length:         1679
Score:                  635.00        Matches:        147
Percent Similarity:     54.72%        Conservative:   50
Best Local Similarity:  40.83%        Mismatches:     145
Query Match:            29.52%        Indels:         18
DB:                     1             Gaps:           8

US-09-101-518A-2 (1-415) x US-08-202-056-6 (1-1679)

Qy     67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
          |||||||||           :::         |||      :::|||   :::|||
Db    399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy     83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
          |||      :::      ||||||                    :::|||
Db    459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy    100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
              |||:::|||      |||||||||:::|||||||||||||:::::::||||||
Db    519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy    120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
             |||      :::|||          |||         |||||||||:::|||||||||
Db    579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy    140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
             ||||||||||||||||||   |||||||||      ||||||             :::
Db    639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy    160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
             :::|||   ||||||   |||:::   |||||||||         ||||||
Db    699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy    180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
          :::|||||||||      :::||||||||||||||||:::   ||||||||||||
Db    759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy    200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
          ||||||||||||         ||||||                :::   :::||||||
Db    819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
              :::|||   :::      |||   |||||||||:::   :::|||
Db    879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy    238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                ||||||:::      |||           |||   ::::::
Db    939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy    257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                |||             |||   |||      ||||||||||||||
Db    993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052
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Qy    273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db   1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy    292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
Db   1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy    312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
Db   1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy    332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
Db   1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy    352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
Db   1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
Db   1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy    392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
Db   1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469
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RESULT 6
US-08-076-093A-5
; Sequence 5, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-076-093A-5

Alignment Scores:

Pred. No.:	3.36e-61	Length:	1679
Score:	635.00	Matches:	147
Percent Similarity:	54.72%	Conservative:	50
Best Local Similarity:	40.83%	Mismatches:	145
Query Match:	29.52%	Indels:	18
DB:	1	Gaps:	8

US-09-101-518A-2 (1-415) x US-08-076-093A-5 (1-1679)

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Qy     67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
Db    399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy     83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
Db    459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy    100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
Db    519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy    120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db    579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy    140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
Db    639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy    160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db    699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy    180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db    759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy    200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db    819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
Db    879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy    238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGln 256
Db    939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy    257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db    993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy    273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db   1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy    292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
Db   1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy    312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
Db   1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy    332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
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Db   1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy    352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
          ||||||      ||||||||||||||||||:::||||||   |||   ||||||||
Db   1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
          ||||||      :::      ||||||   :::||||||||||                |||
Db   1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy    392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
          :::         |||   ||||||   ||||||   |||||||:::     |||:::
Db   1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 7
US-08-701-265-5
; Sequence 5, Application US/08701265
; Patent No. 5776457
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,265
;      FILING DATE:  22-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-701-265-5

Alignment Scores:
Pred. No.:              3.36e-61        Length:         1679
Score:                  635.00          Matches:        147
Percent Similarity:     54.72%          Conservative:   50
Best Local Similarity:  40.83%          Mismatches:     145
Query Match:            29.52%          Indels:         18
DB:                     1               Gaps:           8
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US-09-101-518A-2 (1-415) x US-08-701-265-5 (1-1679)

Qy     67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
          |||||||||            :::         |||      :::|||   :::|||
Db    399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy     83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
          |||         :::      ||||||                        :::|||
Db    459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy    100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
          |||:::|||      ||||||||||:::||||||||||||:::::||||||
Db    519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy    120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
          |||      :::|||         |||         |||||||||:::||||||||||
Db    579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy    140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
          ||||||||||||||||||   |||||||||      ||||||            :::
Db    639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy    160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
          :::|||   ||||||   |||:::   |||||||||          ||||||
Db    699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy    180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
          :::|||||||||      :::||||||||||||||||||:::   ||||||||||||
Db    759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy    200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
          ||||||||||||         ||||||                  :::   :::||||||
Db    819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
          :::|||   :::      |||   |||||||||:::   :::|||
Db    879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy    238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                ||||||:::      |||           |||   ::::::
Db    939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy    257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                |||                |||   |||      ||||||||||||||
Db    993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy    273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
          ||||||:::|||||||||   :::||||||      ::::::      |||
Db   1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy    292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
          |||      :::|||   :::|||:::|||:::   :::::::|||         |||
Db   1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy    312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
          |||||||||:::|||||||||:::|||:::   :::|||   |||      |||
Db   1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy    332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
          |||:::   |||         :::   ||||||   ::::::
Db   1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy    352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
          ||||||      ||||||||||||||||||:::||||||   |||   ||||||||
Db   1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
          ||||||      :::      ||||||   :::||||||||||                |||
Db   1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy    392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
          :::         |||   ||||||   ||||||   |||||||:::     |||:::
Db   1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469
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RESULT 8
US-08-284-586-5
; Sequence 5, Application US/08284586
; Patent No. 5840856
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,586
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-284-586-5

Alignment Scores:
Pred. No.:              3.36e-61        Length:         1679
Score:                  635.00          Matches:        147
Percent Similarity:     54.72%          Conservative:   50
Best Local Similarity:  40.83%          Mismatches:     145
Query Match:            29.52%          Indels:         18
DB:                     2               Gaps:           8

US-09-101-518A-2 (1-415) x US-08-284-586-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||           :::         |||      :::|||   :::|||
Db     399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
           |||       :::      ||||||                        :::|||
Db     459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
               |||:::|||      |||||||||:::|||||||||||||:::::::||||||
Db     519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
           |||      :::|||         |||         |||||||||:::|||||||||
Db     579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
           ||||||||||||||||||   |||||||||      ||||||             :::
Db     639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
           :::|||   ||||||   |||:::   |||||||||         ||||||
Db     699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
           :::|||||||||      :::||||||||||||||||||:::   ||||||||||||
Db     759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
           ||||||||||||      ||||||                  :::   :::||||||
Db     819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
               :::|||   :::      |||   |||||||||:::   :::|||   .
Db     879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                  ||||||:::      |||            |||   ::::::
Db     939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                  |||                |||   |||      ||||||||||||||
Db     993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::|||||||||   :::||||||      ::::::      |||
Db    1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
           |||      :::|||   :::|||:::|||:::   :::::::|||         |||
Db    1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
           ||||||||:::||||||||:::|||:::   :::|||   |||      |||
Db    1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
           |||:::        |||            :::   ||||||   ::::::
Db    1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
           ||||||      ||||||||||||||||||:::||||||   |||   |||||||||
Db    1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::|||||||||              |||
Db    1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
           :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db    1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 9
US-08-805-478-5
; Sequence 5, Application US/08805478
; Patent No. 5874543
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,478
;      FILING DATE:  25-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-805-478-5

Alignment Scores:
Pred. No.:                3.36e-61      Length:          1679
Score:                    635.00        Matches:         147
Percent Similarity:       54.72%        Conservative:    50
Best Local Similarity:    40.83%        Mismatches:      145
Query Match:              29.52%        Indels:          18
DB:                       2             Gaps:            8

US-09-101-518A-2 (1-415) x US-08-805-478-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||            :::          |||       :::|||   :::|||
Db     399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
           |||          :::      ||||||                          :::|||
Db     459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
           |||:::|||      ||||||||||:::|||||||||||||:::::||||||
Db     519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
           |||       :::|||          |||          |||||||||:::||||||||||
Db     579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
           ||||||||||||||||   |||||||||      ||||||                 :::
Db     639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
           :::|||   ||||||   |||:::   |||||||||          ||||||
Db     699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
           :::|||||||||      :::||||||||||||||||||:::   ||||||||||
Db     759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
           ||||||||||||         ||||||                  :::   :::||||||
Db     819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
               :::|||   :::      |||   |||||||||:::   :::|||
Db     879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                  |||||:::      |||          |||   ::::::
Db     939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                  |||                |||   |||      ||||||||||||||
Db     993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::|||||||||   :::|||||      ::::::      |||
Db    1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
           |||      :::|||   :::|||:::|||:::   :::::::|||         |||
Db    1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
           |||||||||:::|||||||||:::|||:::   :::|||   |||      |||
Db    1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysServalThrSer 351
           |||:::        |||             :::   ||||||   ::::::
Db    1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
           ||||||      ||||||||||||||||||:::||||||   |||   |||||||||
Db    1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::||||||||||                |||
Db    1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
           :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db    1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 10
US-08-802-627A-5
; Sequence 5, Application US/08802627A
; Patent No. 5892017
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,627A
;      FILING DATE:  19-Feb-1997
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;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-802-627A-5

Alignment Scores:
Pred. No.:              3.36e-61      Length:          1679
Score:                  635.00        Matches:         147
Percent Similarity:     54.72%        Conservative:    50
Best Local Similarity:  40.83%        Mismatches:      145
Query Match:            29.52%        Indels:          18
DB:                     2             Gaps:            8

US-09-101-518A-2 (1-415) x US-08-802-627A-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||           :::         |||      :::|||   :::|||
Db     399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
           |||         :::      ||||||                          :::|||
Db     459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
               |||:::|||      |||||||||:::||||||||||||:::::::||||||
Db     519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
           |||      :::|||         |||         |||||||||:::|||||||||
Db     579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
              ||||||||||||||||||   ||||||||      ||||||             :::
Db     639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
           :::|||   ||||||   |||:::   |||||||||         ||||||
Db     699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
           :::|||||||||      :::||||||||||||||||||:::   ||||||||||||
Db     759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
           ||||||||||||         ||||||                  :::   :::||||||
Db     819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
              :::|||   :::      |||   |||||||||:::   :::|||
Db     879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                  ||||||:::      |||           |||   ::::::
Db     939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                  |||                  |||   |||      ||||||||||||||
Db     993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::|||||||||   :::||||||      ::::::      |||
Db    1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
              |||      :::|||   :::|||:::|||:::   :::::::|||         |||
Db    1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
           |||||||||:::|||||||||:::|||:::   :::|||   |||      |||
Db    1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
           |||:::         |||                :::   ||||||   ::::::
Db    1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
           ||||||      ||||||||||||||||||:::||||||   |||   |||||||||
Db    1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::|||||||||                |||
Db    1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
              :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db    1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 11
US-08-801-238-5
; Sequence 5, Application US/08801238
; Patent No. 5919896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,238
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D1
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-801-238-5

Alignment Scores:
Pred. No.:              3.36e-61      Length:        1679
Score:                  635.00        Matches:       147
Percent Similarity:     54.72%        Conservative:  50
Best Local Similarity:  40.83%        Mismatches:    145
Query Match:            29.52%        Indels:        18
DB:                     2             Gaps:          8

US-09-101-518A-2 (1-415) x US-08-801-238-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||             :::         |||     :::|||   :::|||
Db     399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
           |||         :::      ||||||                      :::|||
Db     459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
           |||:::|||      |||||||||:::||||||||||||:::::::||||||
Db     519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
           |||      :::|||         |||         |||||||||:::|||||||||
Db     579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
           ||||||||||||||||||   |||||||||      ||||||           :::
Db     639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
           :::|||   ||||||   |||:::   |||||||||         ||||||
Db     699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
           :::||||||||||      :::||||||||||||||||||:::   ||||||||||||
Db     759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
           ||||||||||||        ||||||                :::   :::||||||
Db     819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
           :::|||   :::      |||   ||||||||||:::   :::|||
Db     879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                ||||||:::      |||           |||   ::::::
Db     939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
           |||                     |||   |||      ||||||||||||||||
Db     993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::|||||||||   :::||||||      ::::::      |||
Db    1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
           |||      :::|||   :::|||:::|||:::   ::::::|||         |||
Db    1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
           |||||||||:::|||||||||:::|||:::   :::|||   |||      |||
Db    1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
           |||:::         |||               :::   ||||||   ::::::
Db    1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
           ||||||      ||||||||||||||||||:::||||||   |||   |||||||||
Db    1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::|||||||||                |||
Db    1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
           :::         |||   ||||||   ||||||   |||||||:::      |||:::
Db    1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 12
US-08-801-228-5
; Sequence 5, Application US/08801228
; Patent No. 5922541
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  METHODS FOR DETECTION AND AMPLIFICATION OF
;    TITLE OF INVENTION:  PF4A RECEPTOR NUCLEIC ACID
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,228
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-801-228-5

Alignment Scores:
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```
Pred. No.:              3.36e-61        Length:         1679
Score:                  635.00          Matches:        147
Percent Similarity:     54.72%          Conservative:   50
Best Local Similarity:  40.83%          Mismatches:     145
Query Match:            29.52%          Indels:         18
DB:                     2               Gaps:           8

US-09-101-518A-2 (1-415) x US-08-801-228-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||           :::          |||      :::|||   :::|||
Db     399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
           |||         :::      ||||||                         :::|||
Db     459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
               |||:::|||      ||||||||:::||||||||||||:::::::||||||
Db     519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
              |||      :::|||         |||         |||||||||:::|||||||||
Db     579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
              |||||||||||||||||   ||||||||||      ||||||             :::
Db     639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
              :::|||   ||||||   |||:::   ||||||||            ||||||
Db     699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
           :::||||||||||      :::|||||||||||||||||||:::   ||||||||||||
Db     759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
           ||||||||||||         ||||||                    :::   :::||||||
Db     819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
              :::|||   :::      |||   |||||||||:::   :::|||
Db     879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
                  ||||||:::      |||         |||   ::::::
Db     939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                  |||                  |||   |||      ||||||||||||||
Db     993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::||||||||||   :::||||||      ::::::      |||
Db    1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
              |||      :::|||   :::|||:::|||:::   ::::::|||         |||
Db    1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
              |||||||||:::|||||||||:::|||:::   :::|||   |||      |||
Db    1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
           |||:::         |||                :::   ||||||   ::::::
Db    1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
              ||||||      ||||||||||||||||||:::||||||   |||   |||||||||
Db    1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::|||||||||               |||
Db    1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
              :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db    1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 13
US-09-104-296-5
; Sequence 5, Application US/09104296
; Patent No. 6087475
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/104,296
;      FILING DATE:  24-June-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/701265
;      FILING DATE:  22-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/664228
;      FILING DATE:  06-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-09-104-296-5

Alignment Scores:
Pred. No.:              3.36e-61        Length:         1679
Score:                  635.00          Matches:        147
Percent Similarity:     54.72%          Conservative:   50
Best Local Similarity:  40.83%          Mismatches:     145
Query Match:            29.52%          Indels:         18
DB:                     3               Gaps:           8

US-09-101-518A-2 (1-415) x US-09-104-296-5 (1-1679)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
           |||||||||           :::          |||      :::|||   :::|||
```

```
Db    399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy     83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
          |||        :::      ||||||                    :::|||
Db    459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy    100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
             |||:::|||      ||||||||||:::||||||||||||:::::||||||
Db    519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy    120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
             |||      :::|||         |||         |||||||||:::|||||||||
Db    579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy    140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
          ||||||||||||||||||   |||||||||      ||||||           :::
Db    639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698

Qy    160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
             :::|||   ||||||   |||:::   |||||||||        ||||||
Db    699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy    180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
          :::||||||||      :::||||||||||||||||||:::   ||||||||||||
Db    759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy    200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
          ||||||||||||        ||||||                :::   :::||||||
Db    819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
             :::|||   :::      |||   ||||||||||:::   :::|||
Db    879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy    238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGln 256
                |||||:::      |||            |||   ::::::
Db    939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy    257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                |||                |||   |||      ||||||||||||||
Db    993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy    273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
          ||||||:::||||||||   :::||||||      ::::::      |||
Db   1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy    292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
             |||      :::|||   :::|||:::|||:::   :::::::|||         |||
Db   1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy    312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
          |||||||||:::||||||||||:::|||:::   :::|||   |||      |||
Db   1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy    332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
          |||:::        |||               :::   ||||||   ::::::
Db   1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy    352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
             ||||||      ||||||||||||||||||:::||||||   |||   ||||||||
Db   1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
          ||||||      :::      ||||||   :::|||||||||                |||
Db   1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy    392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
             :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db   1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 14
PCT-US94-06380-3
; Sequence 3, Application PC/TUS9406380
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  K. Jin Kim
;    APPLICANT:  Genentech, Inc.
;    TITLE OF INVENTION:  METHODS FOR TREATING INFLAMMATORY DISRODERS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/06380
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US94-06380-3

Alignment Scores:
Pred. No.:                3.36e-61      Length:          1679
Score:                    635.00        Matches:         147
Percent Similarity:       54.72%        Conservative:    50
Best Local Similarity:    40.83%        Mismatches:      145
Query Match:              29.52%        Indels:          18
DB:                       5             Gaps:            8

US-09-101-518A-2 (1-415) x PCT-US94-06380-3 (1-1679)

Qy     67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
          |||||||||             :::         |||      :::|||   :::|||
Db    399 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 458

Qy     83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
          |||        :::      ||||||                    :::|||
Db    459 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGGCCCCTCATGGCCTCCTTCAAG 518

Qy    100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
             |||:::|||      ||||||||||:::||||||||||||:::::||||||
Db    519 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 578

Qy    120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
             |||      :::|||         |||         |||||||||:::|||||||||
Db    579 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 638

Qy    140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
          ||||||||||||||||||   |||||||||      ||||||           :::
Db    639 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 698
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```
Qy    160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db    699 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 758

Qy    180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db    759 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 818

Qy    200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db    819 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 878

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
Db    879 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 938

Qy    238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGln 256
Db    939 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 992

Qy    257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db    993 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 1052

Qy    273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db   1053 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 1112

Qy    292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
Db   1113 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 1172

Qy    312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
Db   1173 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 1232

Qy    332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
Db   1233 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 1292

Qy    352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
Db   1293 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 1352

Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
Db   1353 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1412

Qy    392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
Db   1413 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1469

RESULT 15
US-08-202-056-8
; Sequence 8, Application US/08202056
; Patent No. 5440021
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Lee, James
;    TITLE OF INVENTION:  Antibodies to Human IL-8 Type B Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,056
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1748 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-202-056-8

Alignment Scores:
Pred. No.:                3.58e-61      Length:          1748
Score:                    635.00        Matches:         146
Percent Similarity:       53.56%        Conservative:    57
Best Local Similarity:    38.52%        Mismatches:      136
Query Match:              29.52%        Indels:          40
DB:                       1             Gaps:            8

US-09-101-518A-2 (1-415) x US-08-202-056-8 (1-1748)

Qy     50 SerGlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsn 69
Db     46 TCAAAAATGGAAGATTTTAACATGGAGAGTGACAGC--------------TTTGAAGAT 90

Qy     70 Phe---------------SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCys 84
Db     91 TTCTGGAAAGGTGAAGATCTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTA 150

Qy     85 CysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuPro 104
Db    151 CTAGATGCCGCCCCATGTGAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTC 207

Qy    105 AlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaVal 124
Db    208 ATTATCTATGCCCTGGTATTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTC 267

Qy    125 LeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaVal 144
Db    268 ATCTTATACAGCAGGGTCGGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTG 327

Qy    145 AlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrp 164
Db    328 GCCGACCTACTCTTTGCCCTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGG 387

Qy    165 ValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAla 184
Db    388 ATTTTTGGCACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGT 447

Qy    185 GlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr 204
Db    448 GGCATCCTGCTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACA 507

Qy    205 GlnLeuTyrArgArgGlyProProAlaArgValThrLeuThr------------------ 218
Db    508 CGC----------------------------ACACTGACCCAGAAGCGCTACTTGGTC 537

Qy    219 ---------CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
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Db    538 AAATTCATATGTCTCAGCATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTT 597

Qy    236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
          |||       :::       ::::::         |||       :::
Db    598 TTCCGAAGGACCGTCTACTCATCCAATGTTAGCCCAGCC---TGC---------TATGAG 645

Qy    256 GlnValGly----------------ArgThrAlaLeuArgValLeuGlnLeuValAla 269
            :::|||                 |||     ||||||:::|||
Db    646 GACATGGGCAACAATACAGCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTT 705

Qy    270 GlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
          ||||||:::::|||||||||:::|||   :::||||||         |||      |||
Db    706 GGCTTCATCGTGCCACTGCTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTG 765

Qy    290 LeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValVal 309
          :::       ::::::   ||||||||||||:::::      |||||||:::
Db    766 TTTAAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTC 825

Qy    310 AlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAsp 329
            |||   |||||||||   ||||||:::||||||:::|||   |||   ||||||
Db    826 ATCTTCCTGCTTTGCTGGCTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGG 885

Qy    330 LeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
                :::         |||   |||   :::   :::|||   |||
Db    886 ACCCAGGTGATCCAGGAGACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCC 945

Qy    350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
          |||       ||||||   :::|||   |||||||||||||||:::|||||||||:::|||
Db    946 ACCGAGATTCTGGGCATCCTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGC 1005

Qy    370 ValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArg 389
            |||||||||       :::       :::|||.         |||      ::::::
Db   1006 CAGAAGTTTCGCCATGGACTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGAC 1065

Qy    390 GlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
            |||   :::             |||         ||||||         ||||||
Db   1066 TCCCTGCCCAAAGACAGCAGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1122


Search completed: November  2, 2002, 12:20:16
Job time : 73 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 06:28:13 ; Search time 66 Seconds
(without alignments)
698.419 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2142	99.6	415	18	AAW19780	Human G-protein ch
2	2136	99.3	472	22	AAG75628	Human colon cancer
3	1909	88.7	378	20	AAY50129	Human chemokine re
4	1891	87.9	368	19	AAW54371	Human IP-10/Mig re
5	1891	87.9	368	21	AAY90614	Human G protein-co
6	1891	87.9	368	22	AAG80122	Human CXCR3 protei
7	1885	87.6	368	21	AAY90648	Human mutant G pro
8	1626.5	75.6	367	19	AAW69999	Rodent chemokine r
9	640	29.8	374	20	AAY06643	Mouse Burkitt's ly
10	637.5	29.6	399	22	ABG13609	Novel human diagno
11	637.5	29.6	399	22	ABB12024	Human IL-8R B homo
12	635	29.5	372	13	AAR27793	New platelet facto
13	635	29.5	372	16	AAR92239	Chemokine superfam
14	635	29.5	372	16	AAR68813	Human lymphocyte P
15	635	29.5	372	20	AAY06644	Human Burkitt's ly
16	635	29.5	372	21	AAY90627	Human G protein-co
17	635	29.5	372	22	AAG80124	Human CXCR5 protei
18	635	29.5	378	22	ABB11873	Human Burkitt lymp
19	633	29.4	355	14	AAR33420	Human IL-8 recepto
20	633	29.4	355	17	AAB09990	Human IL-8 recepto
21	633	29.4	360	13	AAR28273	Sequence in a low
22	633	29.4	360	16	AAR80758	Interleukin 8 rece
23	633	29.4	360	22	AAG80121	Human CXCR2 protei
24	633	29.4	372	21	AAY90661	Human mutant G pro
25	626.5	29.1	1064	16	AAR70124	IL8-R type 2-GBP 1
26	618	28.7	360	16	AAR80953	Recombinant high a
27	615.5	28.6	355	13	AAR28272	Sequence in a high
28	615.5	28.6	355	16	AAR80950	Recombinant high a
29	615	28.6	358	16	AAR80952	Recombinant high a
30	605.5	28.1	350	16	AAR68811	Interleukin-8 rece
31	605.5	28.1	350	16	AAR80756	Interleukin 8 rece
32	605.5	28.1	350	16	AAR80951	Recombinant high a
33	605.5	28.1	350	17	AAB09989	Human IL-8 recepto
34	605.5	28.1	350	22	AAG80120	Human CXCR1 protei
35	605.5	28.1	1060	16	AAR70123	IL8-R type 1-GBP 1
36	600.5	27.9	350	13	AAR27791	Interleukin-8 rece
37	589.5	27.4	410	15	AAR53743	Putative seven tra
38	589.5	27.4	410	19	AAW48723	Polypeptide sequen
39	589.5	27.4	410	21	AAB21687	Genomic clone of 7
40	588.5	27.4	569	22	ABG12373	Novel human diagno
41	586	27.2	358	15	AAR53745	Partial sequence o
42	586	27.2	358	21	AAB21689	Human 7TM receptor
43	586	27.2	378	19	AAW48724	Human V31 seven tr
44	586	27.2	378	21	AAB21688	Human 7TM receptor
45	586	27.2	378	21	AAY90629	Human G protein-co

ALIGNMENTS

RESULT 1
AAW19780
ID AAW19780 standard; Protein; 415 AA.
XX
AC AAW19780;
XX
DT 28-SEP-1997 (first entry)
XX
DE Human G-protein chemokine receptor HSATU68.
XX
KW HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;
KW signal transduction; therapy; diagnosis; agonist; antagonist;
KW antibody.
XX
OS Homo sapiens.
XX
PN WO9725340-A1.
XX
PD 17-JUL-1997.
XX
PF 11-JAN-1996; 96WO-US00499.
XX
PR 11-JAN-1996; 96WO-US00499.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y;
XX
DR WPI; 1997-372810/34.
DR N-PSDB; AAT72800.
XX
PT DNA encoding new isolated human G-protein chemokine receptor - used
PT to develop products for treating, e.g. autoimmune diseases, chronic
PT infections, allergy, malignancy, inflammation or shock

```
XX
PS   Claim 13; Fig 1a-d; 54pp; English.
XX
CC   A newly identified human 7-transmembrane receptor (AAW19780) has been
CC   putatively identified as a chemokine receptor and has been
CC   designated G-protein chemokine receptor or HSATU68.  Its amino
CC   acid sequence was deduced from a cDNA clone (AAT72800) obtd. from an
CC   activated T-cell library.  The protein shows 39.31% identity and
CC   58.405% similarity to human interleukin-8 receptor.  Recombinant
CC   HSATU68 can be expressed in prokaryotic or eukaryotic host cells
CC   and used to raise antibodies or to screen for agonists or
CC   antagonists useful in the treatment of conditions associated with
CC   chemokine receptor under- or overexpression.  Gene therapy can be
CC   used to express HSATU68 in vivo as a means of treating conditions
CC   related to receptor underexpression.
XX
SQ   Sequence   415 AA;

  Query Match             99.6%;  Score 2142;  DB 18;  Length 415;
  Best Local Similarity   99.8%;  Pred. No. 1.2e-236;
  Matches  414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALNSLLFLLGLLGNGA 120

Qy     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180

Qy     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240

Qy     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300

Qy     301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360

Qy     361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415


RESULT 2
AAG75628
ID   AAG75628 standard; Protein; 472 AA.
XX
AC   AAG75628;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen protein SEQ ID NO:6392.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 8.
XX
OS   Homo sapiens.
XX
PN   WO200122920-A2.
XX
PD   05-APR-2001.
XX
PF   28-SEP-2000; 2000WO-US26524.
XX
PR   29-SEP-1999;   99US-0157137.
PR   03-NOV-1999;   99US-0163280.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Birse CE,  Rosen CA;
XX
DR   WPI; 2001-235357/24.
DR   N-PSDB; AAH35033.
XX
PT   Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT   useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS   Claim 11; Page 7873-7875; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where
CC   the proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene
CC   therapy and vaccine production. N and P may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate P
CC   expression. For example, N and P may be used to treat disorders
CC   associated with decreased expression by rectifying mutations or deletions
CC   in a patient's genome that affect the activity of P by expressing
CC   inactive proteins or to supplement the patients own production of P.
CC   Additionally, N may be used to produce the colon cancer-associated Ps,
CC   by inserting the nucleic acids into a host cell and culturing the cell
CC   to express the proteins. N and P can be used in the prevention, diagnosis
CC   and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC   and AAB77789 represent sequences used in the exemplification of the
CC   present invention.
CC   N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC   missing at time of publication, meaning no sequences are present for
CC   SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ   Sequence   472 AA;

  Query Match             99.3%;  Score 2136;  DB 22;  Length 472;
  Best Local Similarity   99.5%;  Pred. No. 6.9e-236;
  Matches  413;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      58 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 117

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
           |||||||||||||||||||||| |||||||||||||||||| ||||||||||||
Db     118 AEVAALLENFSSSYDYGENESXSCCTSPPCPQDFSLNFDRAFLPALXSLLFLLGLLGNGA 177

Qy     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 237

Qy     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 297

Qy     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 357

Qy     301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 417

Qy     361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 472


RESULT 3
AAY50129
ID   AAY50129 standard; Protein; 378 AA.
XX
```

```
AC   AAY50129;
XX
DT   31-JAN-2000  (first entry)
XX
DE   Human chemokine receptor CXCR3b.
XX
KW   Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
KW   seven transmembrane; G-protein coupled; CXC; IP10; Mig; T-lymphocyte;
KW   recruitment; selective; activated; T-cell; neutrophil; inflammation;
KW   tissue distribution; therapy; rheumatoid arthritis; psoriasis;
KW   multiple sclerosis; transplantation; atherosclerosis; restenosis;
KW   cytokine; delayed type hypersensitivity reaction.
XX
OS   Homo sapiens.
XX
PN   WO9950299-A1.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-SE00501.
XX
PR   30-MAR-1998;   98SE-0001098.
XX
PA   (ASTR ) ASTRA PHARM LTD.
PA   (ASTR ) ASTRA AB.
XX
PI   Delaney S;
XX
DR   WPI; 1999-633638/54.
DR   N-PSDB; AAZ32713.
XX
PT   New polynucleotide encoding a variant chemokine receptor -
XX
PS   Claim 6; Fig 4; 18pp; English.
XX
CC   This sequence represents human chemokine receptor CXCR3b, a splice
CC   variant of chemokine receptor CXCR3 (also referred to as CXCR3a).
CC   Chemokines are a family of small cytokines which bring about the
CC   recruitment of leukocytes during inflammation. The CXC chemokines
CC   mostly attract neutrophils, while the CC chemokines are less selective.
CC   All chemokine receptors are seven transmembrane G-protein coupled
CC   receptors and most are receptors for a number of chemokines, CXCR3a
CC   being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is
CC   expressed in activated, but not in resting T-lymphocytes, and may
CC   therefore play an important role in the selective recruitment of
CC   T-cells which occurs in T-cell mediated inflammatory conditions.
CC   CXCR3b may have an altered pattern of tissue distribution and
CC   function in the inflammatory process. Cells expressing the active
CC   CXCR3b are useful for identifying ligands, especially agonists and
CC   antagonists, of a chemokine receptor. In addition, the receptor
CC   facilitates identification of chemokines responsible for mediating
CC   inflammation reactions via interaction with CXCR3b. The modulation
CC   of inflammatory responses is of therapeutic benefit in many conditions
CC   such as rheumatoid arthritis, psoriasis, multiple sclerosis,
CC   transplantation, delayed type hypersensitivity reactions, atherosclerosis
CC   and restenosis.
XX
SQ   Sequence   378 AA;

  Query Match             88.7%;  Score 1909;  DB 20;  Length 378;
  Best Local Similarity   97.4%;  Pred. No. 5.6e-210;
  Matches  370;  Conservative    2;  Mismatches    6;  Indels    2;  Gaps    1;

Qy      36 LPGLYTAPSSPFPPSQVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS 95
           :|||  :| |  |   ||||||||||||||||||||||||||||||||||||||||||
Db       1 MPGLAHSPGS--PQGWVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS 58

Qy      96 LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPL 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      59 LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPL 118

Qy     156 WAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARV 215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     119 WAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARV 178

Qy     216 TLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPL 275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     179 TLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPL 238

Qy     276 LVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALAR 335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     239 LVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALAR 298

Qy     336 NCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQP 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     299 NCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQP 358

Qy     396 SSSRRDSSWSETSEASYSGL 415
           ||||||||||||||||||||
Db     359 SSSRRDSSWSETSEASYSGL 378


RESULT 4
AAW54371
ID   AAW54371 standard; Protein; 368 AA.
XX
AC   AAW54371;
XX
DT   14-AUG-1998  (first entry)
XX
DE   Human IP-10/Mig receptor CXCR3 protein.
XX
KW   chemokine receptor; cellular signal; treatment; T cell; antitumour;
KW   antiviral; inflammatory disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   22
FT                   /note= "N-linked glycosylation site"
FT   Modified-site   32
FT                   /note= "N-linked glycosylation site""
FT   Domain          59..79
FT                   /note= "TM1 transmembrane domain"
FT   Domain          91..111
FT                   /note= "TM2 transmembrane domain"
FT   Domain          127..147
FT                   /note= "TM3 transmembrane domain"
FT   Domain          170..190
FT                   /note= "TM4 transmembrane domain"
FT   Modified-site   199
FT                   /note= "N-linked glycosylation site"
FT   Domain          224..244
FT                   /note= "TM5 transmembrane domain"
FT   Domain          257..277
FT                   /note= "TM6 transmembrane domain"
FT   Domain          302..322
FT                   /note= "TM7 transmembrane domain"
XX
PN   WO9811218-A1.
XX
PD   19-MAR-1998.
XX
PF   10-SEP-1997;   97WO-US15915.
XX
PR   31-MAR-1997;   97US-0829839.
PR   10-SEP-1996;   96US-0709838.
XX
PA   (KOCH-) KOCHER INST THEODOR.
PA   (LEUK-) LEUKOSITE INC.
XX
PI   Loetscher M,  Mackay CR,  Moser B,  Qin S;
XX
DR   WPI; 1998-207381/18.
DR   N-PSDB; AAV26557.
XX
```

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PT   DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT   which, are useful for treatment of inflammation or in anti-tumour or
PT   anti-viral therapy
XX
PS   Claim 7; Fig 2; 137pp; English.
XX
CC   The mammalian CXC chemokine receptor 3 (CXCR3) protein can selectively
CC   bind one or more chemokines and can mediate cellular signalling and/or a
CC   cellular response in response.  Inhibitors and promoters of mammalian
CC   CXCR3 can be detected and identified using host cells expressing CXCR3.
CC   CXCR3 inhibitors can be used for treatment of inflammatory diseases which
CC   are T cell  mediated.  CXCR3 promoters are useful for antitumour or
CC   antiviral therapy.
XX
SQ   Sequence   368 AA;

  Query Match             87.9%;  Score 1891;  DB 19;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 6.3e-208;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 5
AAY90614
ID   AAY90614 standard; Protein; 368 AA.
XX
AC   AAY90614;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human G protein-coupled receptor GPR9.
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   N-PSDB; AAA30593.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents -
XX
PS   Example 1; Page 116-117; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. The present sequence represents a human wild-type GPCR referred
CC   to in an exemplification of the invention.
XX
SQ   Sequence   368 AA;

  Query Match             87.9%;  Score 1891;  DB 21;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 6.3e-208;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 6
```

```
AAG80122
ID   AAG80122 standard; Protein; 368 AA.
XX
AC   AAG80122;
XX
DT   17-JAN-2002  (first entry)
XX
DE   Human CXCR3 protein.
XX
KW   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW   inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW   chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW   antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW   antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200172830-A2.
XX
PD   04-OCT-2001.
XX
PF   02-APR-2001; 2001WO-EP03708.
XX
PR   31-MAR-2000; 2000DE-1016013.
XX
PA   (IPFP-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
XX
PI   Forssmann W,  Adermann K,  Heitland A,  Spodsberg N;
XX
DR   WPI; 2001-626256/72.
XX
PT   Diagnostic agent containing two or more receptor-specific ligands,
PT   useful for detecting tumors, inflammation etc., also therapeutic use of
PT   ligand inhibitors  -
XX
PS   Disclosure; Page 12; 26pp; German.
XX
CC   This invention describes a novel diagnostic agent (A) comprising at least
CC   two different ligands (I) for receptors (II) that are implicated in
CC   disease. (A) are used for the diagnosis of tumors (especially colorectal
CC   or prostatic), organ rejection, inflammation and autoimmune diseases.
CC   Also inhibitors of (I) are used therapeutically against tumors (and their
CC   metastases), inflammation (particularly bronchial asthma or chronic bowel
CC   inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC   where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC   endocrine, motor or urogenital systems or skin are affected, and bone
CC   marrow diseases. The products of the invention are chemokine derivatives
CC   which have cytostatic, antiinflammatory, antiasthmatic,
CC   immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC   Chemokines act on specific tumor and inflammatory cells through a
CC   constellation of chemokine receptors (CR), which control migration and
CC   proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC   fragments used to illustrate the method of the invention.
XX
SQ   Sequence   368 AA;

  Query Match             87.9%;  Score 1891;  DB 22;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 6.3e-208;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 7
AAY90648
ID   AAY90648 standard; Protein; 368 AA.
XX
AC   AAY90648;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human mutant G protein-coupled receptor GPR9 (M254K).
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   N-PSDB; AAA30714.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents  -
XX
PS   Example 2; Page 224-225; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
```

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CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. Sequences AAY90643- AAY90677 and AAY90683-Y90687 the mutant
CC   human GPCRs of the invention.
XX
SQ   Sequence   368 AA;

  Query Match             87.6%;  Score 1885;  DB 21;  Length 368;
  Best Local Similarity   99.5%;  Pred. No. 3.1e-207;
  Matches  363;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAKRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 8
AAW69999
ID   AAW69999 standard; Protein; 367 AA.
XX
AC   AAW69999;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Rodent chemokine receptor HST01.1 amino acid sequence.
XX
KW   Chemokine; primate; human; rodent; chemokine receptor; asthma;
KW   inflammatory response; immune response; leukocyte migration; GPCR;
KW   leukocyte adhesion; chemoattractant; modulation; antiviral response;
KW   cellular morphology modification response; G-protein coupled receptor;
KW   phosphoinositide lipid turnover; abnormal proliferation; regeneration;
KW   atrophy; HST01.1.
XX
OS   Mus sp.
XX
PN   WO9832858-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US00902.
XX
PR   23-JAN-1997;   97US-0036715.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM,  Hedrick JA,  Mattson JD,  Soto-trejo H;
PI   Zlotnik A;
XX
DR   WPI; 1998-427954/36.
DR   N-PSDB; AAV43793.
XX
PT   Rodent and primate chemokines and chemokine receptors - useful
PT   diagnostically and therapeutically to treat conditions associated
PT   with abnormal physiology or development e.g. inflammatory conditions
XX
PS   Claim 4; Pages 89-92; 105pp; English.
XX
CC   This represents a rodent chemokine receptor HST01.1 amino acid sequence.
CC   The invention provides novel primate and rodent chemokines and chemokine
CC   receptors. The chemokines, receptors and binding compounds (optionally
CC   antibodies/fragments specifically binding the chemokines) are useful
CC   therapeutically to treat conditions associated with abnormal physiology
CC   or development e.g. inflammatory conditions such as asthma. Chemokines
CC   are important in immune and inflammatory responses in that they induce
CC   leukocyte migration and adhesion. They are also chemoattractants for
CC   several cells involved in inflammation and can induce other biological
CC   responses e.g. modulation of second messenger levels (e.g. Ca++),
CC   cellular morphology modification responses, phosphoinositide lipid
CC   turnover, possible antiviral responses etc. The chemokine receptors of
CC   the invention exhibit structural properties of G-protein coupled
CC   receptors (GPCR), although their ligands have not yet been identified.
CC   The chemokine and chemokine receptor polypeptides are useful to produce
CC   ligand:receptor complexes in vivo or in assay techniques. Assays may
CC   also involve chemical antagonists which block complex production or
CC   utilise competitive binding.  Binding compounds identified (agonists or
CC   antagonists) can be used to modulate the physiological responses in cells
CC   (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC   proliferation, regeneration, generation and atrophy. The polypeptides
CC   are also used to produce antibodies useful diagnostically, for drug
CC   screening or for polypeptide purification. The polynucleotides are useful
CC   to produce probes for detecting the polypeptides, and to isolate the
CC   polypeptides or related sequences, especially from other species. They
CC   also allow transformation of cells for polypeptide production.
XX
SQ   Sequence   367 AA;

  Query Match             75.6%;  Score 1626.5;  DB 19;  Length 367;
  Best Local Similarity   86.0%;  Pred. No. 1.4e-177;
  Matches  314;  Conservative   22;  Mismatches   28;  Indels    1;  Gaps    1;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||: |||: :: | |||| :| |||||||||    ||||||||||||| |||||||||
Db       4 EVSERQVLDASDFAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL 62

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||:|||||||||||||||| ||||||||||||||||||| ||
Db      63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           |||||||||||||| |||||||||||:||||||:||| |  || |||: |||||||||
Db     123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFA 182

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           |||||:|||:::|:||||||||||||||||||||||||||||||||||||||||||||||
Db     183 LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 242

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||| |||||||||| |||:||||||||||||||:| |||||||:| ||||||||
Db     243 VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRKSHVDVAKSVT 302

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||:|||||||||||||||||:||||  |||  :||| |||||||||:||||||:||
Db     303 SGMGYMHCCLNPLLYAFVGVKFREKMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy     411 SYSGL 415
           || ||
Db     363 SYLGL 367


RESULT 9
AAY06643
```

```
ID   AAY06643 standard; Protein; 374 AA.
XX
AC   AAY06643;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Mouse Burkitt's lymphoma receptor 1 (BLR1).
XX
KW   Burkitt's lymphoma receptor 1; BLR1; mouse;
KW   B lymphocyte chemoattractant; BLC; chemokine; ligand;
KW   drug screening; leukaemia; autoimmune disease; therapy.
XX
OS   Mus musculus.
XX
PN   WO9928468-A1.
XX
PD   10-JUN-1999.
XX
PF   02-DEC-1998;   98WO-US25561.
XX
PR   02-DEC-1997;   97US-0982493.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cyster JG,  Gunn MD,  Williams LT;
XX
DR   WPI; 1999-493764/41.
DR   N-PSDB; AAX87709.
XX
PT   Modulating interaction of a Burkitt's Lymphoma Receptor 1
PT   polypeptide and ligand, useful in drug screens
XX
PS   Claim 1; Page 35; 42pp; English.
XX
CC   This sequence represents mouse Burkitt's lymphoma receptor 1
CC   (BLR1).  The invention relates to methods for modulating the
CC   interaction of BLR1 with its ligand, B lymphocyte chemoattractant
CC   (BLC, see AAY06641).  The methods comprise combining BLR1 and BLC
CC   polypeptides with a candidate modulator agent under conditions
CC   whereby, but for the presence of the agent, the polypeptides engage
CC   in a first interation, and determining a second interaction of the
CC   polypeptides in the presence of the agent, wherein a difference
CC   between the first and second interactions indicates that the agent
CC   modulates the interaction of the polypeptides.  The modulator is
CC   preferably an antagonist, especially dominant negative, form of
CC   BLC.  BLC and BLC agonists and antagonists may be useful for
CC   treating viral (e.g. HIV) infections, lymphoma, B lineage
CC   leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC   thyroiditis and diabetes.
XX
SQ   Sequence   374 AA;

  Query Match             29.8%;  Score 640;  DB 20;  Length 374;
  Best Local Similarity   40.9%;  Pred. No. 2.4e-64;
  Matches  143;  Conservative   54;  Mismatches  139;  Indels   14;  Gaps    6;

Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           :|:| :    :|: | |         :|   |:|  |||:||||::||  |  :|   |
Db      26 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
           |||:||| |||||| |||  ||    : :| || |: |||   ||  ||||  :||:
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLV 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
           |||: |||| ||||   |||     : :|| |:|    |||||: :|      |::: |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
           | ::      |      | |  : |||||:||| :||  ::  ||   |  :| :|:
Db     202 -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |   : | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT 369


RESULT 10
ABG13609
ID   ABG13609 standard; Protein; 399 AA.
XX
AC   ABG13609;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #13600.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS77796.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 43968; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   399 AA;

  Query Match             29.6%;  Score 637.5;  DB 22;  Length 399;
  Best Local Similarity   37.3%;  Pred. No. 5.2e-64;
  Matches  154;  Conservative   57;  Mismatches  145;  Indels   57;  Gaps   10;
```

```
Qy      17 GGAAQSKSQTKSDSITKEFLPGLYTAPSSPFP-PSQVSDHQVLNDAEVAALLENF----- 70
           ||  | ||                  |  | |   |:: |  : :|:      |:|
Db      20 GGVLQVKS----------------PATQSGFKFTSKMEDFNMESDS-----FEDFWKGED 58

Qy      71 SSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRT 130
             |:| |          : ||  : ||  :: |:  :|:|:||| |||| |  |:|  |
Db      59 LSNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRV 117

Qy     131 ALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLA 190
             | || :||:||:|| |  ||||:||      |:||: |||| |  :|||:| ||||
Db     118 GRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLA 177

Qy     191 CISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHH 241
           ||| |||| |||||:          |||         ||::||| || |||  :|    :
Db     178 CISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVY 227

Qy     242 DERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQ 295
             ::   |   :|      | ||:|    ||::|||:| :||   |  |  :
Db     228 SSNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMG 283

Qy     296 RRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGY 355
           :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  ||
Db     284 QKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGI 343

Qy     356 MHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           :| |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db     344 LHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 396
```

RESULT 11
ABB12024
ID ABB12024 standard; peptide; 399 AA.
XX
AC ABB12024;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human IL-8R B homologue, SEQ ID NO:2394.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09268.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 20; Page 298; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.
XX
SQ Sequence 399 AA;

```
  Query Match             29.6%;  Score 637.5;  DB 22;  Length 399;
  Best Local Similarity   37.3%;  Pred. No. 5.2e-64;
  Matches  154;  Conservative   57;  Mismatches  145;  Indels   57;  Gaps   10;

Qy      17 GGAAQSKSQTKSDSITKEFLPGLYTAPSSPFP-PSQVSDHQVLNDAEVAALLENF----- 70
           ||  | ||                  |  | |   |:: |  : :|:      |:|
Db      20 GGVLQVKS----------------PATQSGFKFTSKMEDFNMESDS-----FEDFWKGED 58

Qy      71 SSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRT 130
             |:| |          : ||  : ||  :: |:  :|:|:||| |||| |  |:|  |
Db      59 LSNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRV 117

Qy     131 ALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLA 190
             | || :||:||:|| |  ||||:||      |:||: |||| |  :|||:| ||||
Db     118 GRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLA 177

Qy     191 CISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHH 241
           ||| |||| |||||:          |||         ||::||| || |||  :|    :
Db     178 CISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVY 227

Qy     242 DERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQ 295
             ::   |   :|      | ||:|    ||::|||:| :||   |  |  :
Db     228 SSNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMG 283

Qy     296 RRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGY 355
           :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  ||
Db     284 QKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGI 343
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```
Qy    356 MHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
          :| |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db    344 LHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 396


RESULT 12
AAR27793
ID   AAR27793 standard; Protein; 372 AA.
XX
AC   AAR27793;
XX
DT   12-MAR-1993  (first entry)
XX
DE   New platelet factor 4 receptor superfamily member PF4ARii.
XX
KW   IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
KW   pro-inflammatory cytokine; 8rr.9.
XX
OS   Homo sapiens.
XX
PN   WO9217497-A.
XX
PD   15-OCT-1992.
XX
PF   23-MAR-1992;   92WO-US02317.
XX
PR   29-MAR-1991;   91US-0677211.
PR   19-DEC-1991;   91US-0810782.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Holmes WE,  Lee J,  Wood WI;
XX
DR   WPI; 1992-366191/44.
DR   N-PSDB; AAQ37107.
XX
PT   Isolated human platelet factor 4 super-family receptor
PT   polypeptide and corresp. antibodies and DNA - useful as
PT   diagnostic and screening agents, and for treating inflammation or
PT   PF4AR-mediated disorders
XX
PS   Claim 7; Fig 5; 78pp; English.
XX
CC   The IL-8 receptor cDNA sequence was isolated (see AAQ29505) and a
CC   874bp sub-fragment of the coding sequence was used as a probe to
CC   screen human cell line HL60 and human peripheral blood lymphocyte
CC   cDNA libraries. Two new gene sequences were found that are clearly
CC   related to the IL-8 receptor. One of these was contained in clone
CC   8rr.9 and is predicted to encode an amino acid sequence which is
CC   36% and 38% identical with the high and low affinity IL-8 receptor
CC   sequences, respectively. See also AAQ37107.
XX
SQ   Sequence   372 AA;

  Query Match             29.5%;  Score 635;  DB 13;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 9e-64;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy     67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
          |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db     11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |  |||:||| |||||| |||  ||    : :| || |: |||   ||
Db     71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy    180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
          :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db    131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy    238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
           ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db    191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy    292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
          |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db    249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy    352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 13
AAR92239
ID   AAR92239 standard; Protein; 372 AA.
XX
AC   AAR92239;
XX
DT   26-MAR-1996  (first entry)
XX
DE   Chemokine superfamily receptor.
XX
KW   Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW   rheumatoid arthritis; inflammatory bowel disease;
KW   chronic lung inflammation; treatment; antibody;
KW   affinity purification; detection.
XX
OS   Homo sapiens.
XX
PN   US5440021-A.
XX
PD   08-AUG-1995.
XX
PF   29-MAR-1991;   91US-0677211.
XX
PR   25-FEB-1994;   94US-0202056.
PR   29-MAR-1991;   91US-0677211.
XX
PA   (CHUN/) CHUNTHARAPAI A.
PA   (HEBE/) HEBERT C.
PA   (KIMK/) KIM K J.
PA   (LEEJ/) LEE J.
XX
PI   Chuntharapai A,  Hebert C,  Kim KJ,  Lee J;
XX
DR   WPI; 1995-283151/37.
DR   N-PSDB; AAQ99009.
XX
PT   New antibodies against interleukin 8 type B receptor - used to treat
PT   or prevent inflammation, also for detecting receptor expression and
PT   purificn.
XX
PS   Example 2; Columns 49-52; 62pp; English.
XX
CC   Antibodies directed against the interleukin-8 receptor B can be used
CC   to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC   rheumatoid arthritis and particularly inflammatory bowel disease and
CC   chronic lung inflammation.  When immobilised, these antibodies may
CC   be used to detect interleukin-8 receptor B expression in cells and
CC   tissues and for affinity purification of interleukin-8 receptor B
CC   from cells. This sequence is an additonal chemokine superfamily
CC   receptor which was identified by probing lamda libraries of genomic
CC   DNA from a human monocyte-like cell line (L-60) and human peripheral
CC   blood lymphocytes using a large fragment of the interleukin-8 type
CC   A receptor DNA (See AAQ99006).
XX
SQ   Sequence   372 AA;

  Query Match             29.5%;  Score 635;  DB 16;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 9e-64;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy     67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
          |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db     11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70
```

```
Qy    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
          |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db     71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy    180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
          :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db    131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy    238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
           ||:  |    | ::      |       | |  |||||||:||| :|| ::  |
Db    191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy    292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
          |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db    249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy    352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
```

RESULT 14
AAR68813
ID AAR68813 standard; Protein; 372 AA.
XX
AC AAR68813;
XX
DT 18-JUL-1995 (first entry)
XX
DE Human lymphocyte PF4AR.
XX
KW Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW platelet factor superfamily receptor; lymphocyte; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic.
XX
OS Homo sapiens.
XX
PN WO9428931-A.
XX
PD 22-DEC-1994.
XX
PF 07-JUN-1994; 94WO-US06380.
XX
PR 11-JUN-1993; 93US-0076093.
XX
PA (GETH) GENENTECH INC.
XX
PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
XX
DR WPI; 1995-036114/05.
DR N-PSDB; AAQ80522.
XX
PT Treatment of inflammatory disorders - by administering an
PT antibody capable of binding a platelet factor 4 superfamily
PT receptor polypeptide
XX
PS Disclosure; Page 56-58; 83pp; English.
XX
CC 2 PF4AR members were identified by probing lambda libraries from
CC human monoclyte-like cell line HL-60 and human peripheral blood
CC lymphocytes using a large fragment of IL-8 receptor DNA (full
CC sequence given in AAQ80520). The nucleotide sequences of the 2
CC PF4ARs are given in AAQ80521 and AAQ80522, and their respective
CC amino acid sequences in AAR68812 and AAR68813.
XX
SQ Sequence 372 AA;

Query Match 29.5%; Score 635; DB 16; Length 372;
Best Local Similarity 40.8%; Pred. No. 9e-64;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

```
Qy     67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
          |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db     11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
          |  :|   |   |||:||| |||||| ||| ||    : :| || |: |||   ||
Db     71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy    180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
          :|||  :||||||: |||| ||||   ||      : :|| :| :  | |||: :|
Db    131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy    238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
           ||:  |    | ::      |       | |  |||||||:||| :|| ::  |
Db    191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy    292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
          |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db    249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy    352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
```

RESULT 15
AAY06644
ID AAY06644 standard; Protein; 372 AA.
XX
AC AAY06644;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human Burkitt's lymphoma receptor 1 (BLR1).
XX
KW Burkitt's lymphoma receptor 1; BLR1; human;
KW B lymphocyte chemoattractant; BLC; chemokine; ligand;
KW drug screening; leukaemia; autoimmune disease; therapy.
XX
OS Homo sapiens.
XX
PN WO9928468-A1.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US25561.
XX
PR 02-DEC-1997; 97US-0982493.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cyster JG, Gunn MD, Williams LT;
XX
DR WPI; 1999-493764/41.
DR N-PSDB; AAX87710.
XX
PT Modulating interaction of a Burkitt's Lymphoma Receptor 1
PT polypeptide and ligand, useful in drug screens
XX
PS Claim 1; Page 38; 42pp; English.
XX
CC This sequence represents human Burkitt's lymphoma receptor 1
CC (BLR1). The invention relates to methods for modulating the
CC interaction of BLR1 with its ligand, B lymphocyte chemoattractant
CC (BLC, see AAY06642). The methods comprise combining BLR1 and BLC
CC polypeptides with a candidate modulator agent under conditions
CC whereby, but for the presence of the agent, the polypeptides engage
CC in a first interation, and determining a second interaction of the
CC polypeptides in the presence of the agent, wherein a difference
CC between the first and second interactions indicates that the agent
CC modulates the interaction of the polypeptides. The modulator is
CC preferably an antagonist, especially dominant negative, form of
CC BLC. BLC and BLC agonists and antagonists may be useful for

CC treating viral (e.g. HIV) infections, lymphoma, B lineage
CC leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC thyroiditis and diabetes.
XX
SQ Sequence 372 AA;

Query Match 29.5%; Score 635; DB 20; Length 372;
Best Local Similarity 40.8%; Pred. No. 9e-64;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

```
Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
            |  :|   |  |||:||| |||||| ||| ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :|||||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
             ||:  |    | ::      |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
            |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
```

Search completed: November 2, 2002, 12:04:37
Job time : 69 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:05:20 ; Search time 44 Seconds
(without alignments)
906.297 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1629.5	75.8	367	2	JE0349	interferon-inducib
2	641	29.8	374	2	S32785	G protein-coupled
3	640	29.8	374	2	S42628	G protein-coupled
4	635	29.5	372	2	S26667	G protein-coupled
5	633	29.4	360	2	A53611	interleukin-8 rece
6	631.5	29.4	327	2	S56162	MDCR15 protein - h
7	615.5	28.6	355	2	JQ1231	interleukin-8 rece
8	615	28.6	358	2	A53752	interleukin-8 rece
9	606.5	28.2	350	2	A39445	interleukin-8 rece
10	593.5	27.6	356	2	S42096	interleukin-8 rece
11	586	27.2	378	2	B55735	lymphocyte-specifi
12	582.5	27.1	352	2	G00048	fusin (LESTRA) - c
13	576.5	26.8	352	2	A45747	neuropeptide Y/pep
14	573	26.6	359	2	A48921	interleukin-8 rece
15	571	26.5	353	2	S28787	neuropeptide Y/pep
16	567.5	26.4	378	2	A55735	G protein-coupled
17	566	26.3	378	2	A45680	G protein-coupled
18	563.5	26.2	369	2	JC5068	G protein-coupled
19	551.5	25.6	360	2	A57160	chemokine (C-C) re
20	548	25.5	360	2	JC4587	chemokine (C-C) re
21	536.5	24.9	354	2	B55733	G protein-coupled
22	534.5	24.8	374	2	I38450	chemokine (C-C) re
23	527	24.5	360	2	JC2443	chemokine (C-C) re
24	517	24.0	354	2	A23669	interleukin-8 rece
25	511	23.8	352	2	A43113	chemokine (C-C) re
26	511	23.8	355	2	A45177	chemokine (C-C) re
27	506	23.5	355	2	I49339	macrophage inflamm
28	503.5	23.4	350	2	JN0621	G protein-coupled
29	492.5	22.9	354	2	I58186	probable G protein
30	492	22.9	359	2	I49341	MIP-1 alpha recept
31	491.5	22.8	355	2	G02436	chemokine (C-C) re
32	484	22.5	383	2	S55594	G protein-coupled
33	473.5	22.0	359	2	S15403	angiotensin II rec
34	471.5	21.9	359	2	JQ1516	angiotensin II rec
35	470.5	21.9	359	2	A42656	angiotensin II rec
36	464.5	21.6	355	2	JC4304	orphan G protein-c
37	461	21.4	359	2	JC1104	angiotensin II rec
38	458.5	21.3	359	2	JH0621	angiotensin II rec
39	458.5	21.3	359	2	JC2134	angiotensin II rec
40	456.5	21.2	359	2	S44425	angiotensin II rec
41	454	21.1	359	2	A48857	angiotensin II rec
42	453	21.1	359	2	JC1194	angiotensin II rec
43	452	21.0	362	2	A39714	G protein-coupled
44	447.5	20.8	359	2	I39418	angiotensin II rec
45	447	20.8	362	2	A30341	G protein-coupled

ALIGNMENTS

RESULT 1
JE0349
interferon-inducible protein 10 (IP-10) receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C;Accession: JE0349
R;Tamaru, M.; Tominaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and i
A;Reference number: JE0349; MUID:99009219
A;Accession: JE0349
A;Molecule type: mRNA
A;Residues: 1-367 <TAM>
A;Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732
C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C;Superfamily: vertebrate rhodopsin

Query Match 75.8%; Score 1629.5; DB 2; Length 367;
Best Local Similarity 86.3%; Pred. No. 4e-136;
Matches 315; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

```
Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||: |||: :: | |||| :| |||||||||    ||||||||||||||| |||||||||
Db       4 EVSERQVLDASDFAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL 62

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           |||||||||||||||||:|||||||||||||||| ||||||||||||||||||| ||
Db      63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           |||||||||||||||| ||||||||||:||||||:||| |  || |||: |||||||||
Db     123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFA 182

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           |||||:|||::|:||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 242

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||| |||||||||| |||:||||||||||||||:| ||||||||| ||||||||
Db     243 VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVT 302

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||:|||||||||||||||||:|||| ||| :||| |||||||||:||||||:||
Db     303 SGMGYMHCCLNPLLYAFVGVKFREQMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy     411 SYSGL 415
           || ||
Db     363 SYLGL 367
```

RESULT 2
S32785

```
G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999
C;Accession: S32785
R;Kouba, M.; Vanetti, M.; Wang, X.; Schaefer, M.; Hoellt, V.
FEBS Lett. 321, 173-178, 1993
A;Title: Cloning of a novel putative G-protein-coupled receptor (NLR) which is expressed
A;Reference number: S32785; MUID:93238948
A;Accession: S32785
A;Molecule type: mRNA
A;Residues: 1-374 <KOU>
A;Cross-references: GB:X71463; GB:S59748; NID:g599926; PIDN:CAA50582.1; PID:g599927
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match            29.8%;  Score 641;  DB 2;  Length 374;
  Best Local Similarity  41.7%;  Pred. No. 8.1e-49;
  Matches  146;  Conservative   50;  Mismatches  140;  Indels   14;  Gaps    6;

Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           :|:| :    :|  | |          :|   |:|  |||:||||::||  |  :|   |
Db      26 YSNSTEIPLQDSIFCSTE---EGPLLTSFKTIFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
           |||:||| ||||||| |||  ||    : :| || |: |||   ||  |||| :|||
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLL 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIF---LSAHHDERLN 246
           |||: |||| |||   |||     : :||  :|    ||||| :|   :  |::| |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCSTIWLAGFLFALPELLFAKVVQPHNNESL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
           | ::      |    | | |    |||||:||||:||  ::  ||   |  :| :|:
Db     202 -PQCIFSQENEAETRAWFASRFLYHTGGFLLPMLVMAWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFLLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |     | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPGWRKSSLSESENAT 369


RESULT 3
S42628
G protein-coupled receptor Gpcr6 - mouse
N;Alternate names: interleukin-8 receptor homolog; muBLR1 protein
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
C;Accession: S42628; C48909
R;Kaiser, E.; Foerster, R.; Wolf, I.; Ebensperger, C.; Kuehl, W.M.; Lipp, M.
Eur. J. Immunol. 23, 2532-2539, 1993
A;Title: The G protein-coupled receptor BLR1 is involved in murine B cell differentiatic
A;Reference number: S42628; MUID:94009211
A;Accession: S42628
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-374 <KAI>
A;Cross-references: EMBL:X71788; NID:g2598563; PIDN:CAA50673.1; PID:g433947
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A;Reference number: A48909; MUID:94116980
A;Accession: C48909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 151-269 <WIL>
A;Cross-references: GB:L20332; NID:g438798; PIDN:AAA16852.1; PID:g438799
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match            29.8%;  Score 640;  DB 2;  Length 374;
  Best Local Similarity  40.9%;  Pred. No. 9.9e-49;
  Matches  143;  Conservative   54;  Mismatches  139;  Indels   14;  Gaps    6;

Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           :|:| :    :|: | |          :|   |:|  |||:||||::||  |  :|   |
Db      26 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
           |||:||| ||||||| |||  ||    : :| || |: |||   ||  |||| :|||
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLV 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
           |||: |||| ||||   |||     : :|| |:|   ||||| :|      |::: |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
           | ::      |      | |  : |||||:||| :||  ::  ||   |  :| :|:
Db     202 -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |     | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT 369


RESULT 4
S26667
G protein-coupled receptor BLR1 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S26667
R;Dobner, T.; Wolf, I.; Emrich, T.; Lipp, M.
Eur. J. Immunol. 22, 2795-2799, 1992
A;Title: Differentiation-specific expression of a novel G protein-coupled receptor fr
A;Reference number: S26667; MUID:93049615
A;Accession: S26667
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <DOB>
A;Cross-references: EMBL:X68149; NID:g29459; PIDN:CAA48252.1; PID:g29460
C;Genetics:
A;Gene: GDB:BLR1
A;Cross-references: GDB:136235; OMIM:601613
A;Map position: 15q26.1-15q26.1
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match            29.5%;  Score 635;  DB 2;  Length 372;
  Best Local Similarity  40.8%;  Pred. No. 2.7e-48;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |  |||:||| |||||| ||| ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :||| :|||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::      |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308
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Qy    352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
          ||  |||||||:|| | ||||||  :  || :|||     | :   | || || ||:  |:
Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 5
A53611
interleukin-8 receptor type B - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: I37898; I38712; A53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human interleu
A;Reference number: I37898; MUID:95014476
A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
A;Cross-references: EMBL:U11869; NID:g511801; PIDN:AAB60656.1; PID:g511803
A;Accession: I38712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <RE2>
A;Cross-references: EMBL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873;
11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 rece
A;Reference number: A53611; MUID:94209273
A;Accession: A53611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 6-360 <SPR>
A;Cross-references: GB:M99412; GB:L19593
R;Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
A;Reference number: A39446; MUID:91368200
A;Accession: A39446
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 6-360 <MUR>
A;Cross-references: GB:M73969
C;Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in
C;Genetics:
A;Gene: GDB:IL8RB; IL8RA
A;Cross-references: GDB:127868; OMIM:146928
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             29.4%;  Score 633;  DB 2;  Length 360;
  Best Local Similarity   40.1%;  Pred. No. 3.9e-48;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy     72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
          |:| |          : ||  : ||  :: |:  :|:|:||| ||||  |  |:|  |
Db     21 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79

Qy    132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
           | || :||:||:|| |  ||||:||      |:||: ||||   |  :|||:| |||||
Db     80 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 139

Qy    192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
          || |||| |||||:          |||         ||::||| || |||  :|    :
Db    140 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 189

Qy    243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
          ::   |   :  :|      |  ||:|    ||::|||:| :||   |  |  :   :
Db    190 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 245

Qy    297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
          : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db    246 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 305

Qy    357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
          | |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db    306 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 357


RESULT 6
S56162
MDCR15 protein - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56162
R;Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
Biochem. J. 309, 773-779, 1995
A;Title: Sequence variation of a novel heptahelical leucocyte receptor through altern
A;Reference number: S56162; MUID:95366951
A;Accession: S56162
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-327 <BAR>
A;Cross-references: EMBL:X68829; NID:g840783; PIDN:CAA48723.1; PID:g840784
C;Superfamily: vertebrate rhodopsin

  Query Match             29.4%;  Score 631.5;  DB 2;  Length 327;
  Best Local Similarity   42.7%;  Pred. No. 4.8e-48;
  Matches  138;  Conservative   47;  Mismatches  127;  Indels   11;  Gaps    5;

Qy     97 NFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLW 156
          :|   |:|  |||:||||::||  |  :|   |   |||:||| |||||| |||  ||
Db      3 SFKAVFVPVAYSLIFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFA 62

Qy    157 AVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVT 216
             : :| || |: |||   ||  :|||  :||||||: |||| ||||   ||      :
Db     63 VAEGSVGWVLGTFLCKTVIALHKVNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIH 122

Qy    217 LTCLAVWGLCLLFALPDFIFL---SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVA 269
          :||  :| :  | |||: :|      ||:  |    | ::      |      | |  ||
Db    123 ITCGTIWLVGFLLALPEILFAKVSQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVA 180

Qy    270 GFLLPLLVMAYCYAHILAVL-LVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILM 328
          |||||:||| :||  ::  |    |  :| :|:|: ::|   | |||:|||:|: :| |
Db    181 GFLLPMLVMGWCYVGVVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLA 240

Qy    329 DLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQ 388
          | |:   |      : || ::   ||  ||||||:|| | |||||  :  || :||| :
Db    241 RLKAVDNTCKLNGSLPVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTSP 300

Qy    389 RGLQRQPSSSRRDSSWSETSEAS 411
            | :   | || || ||:  |:
Db    301 ASLCQLFPSWRR-SSLSESENAT 322


RESULT 7
JQ1231
interleukin-8 receptor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Ge
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994
A;Accession: JQ1231
A;Molecule type: DNA
A;Residues: 1-355 <BEC>
A;Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding the rabbit IL-8 recept
A;Reference number: A46483; MUID:92148149
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A;Accession: A46483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-355 <LEE>
A;Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Experimental source: neutrophils
A;Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             28.6%;  Score 615.5;  DB 2;  Length 355;
  Best Local Similarity   38.5%;  Pred. No. 1.4e-46;
  Matches  136;  Conservative   58;  Mismatches  130;  Indels   29;  Gaps    5;

Qy      69 NFSSSYDYGENESDSCCTSPPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVA 122
           |  :  : : |:|  :    ||  :|:|         ::  :  :|:|:||| ||||  |
Db       7 NMTDLWTWFEDEFANATGMPPVEKDYSPCLVVTQTLNKYVVVVIYALVFLLSLLGNSLVM 66

Qy     123 AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
           |:|  |:  | || :||:||:|| |  ||:|:|||     |:||: ||||   :  :||
Db      67 LVILYSRSNRSVTDVYLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSLVKEVNF 126

Qy     183 YAGALLLACISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPD 233
           |:| ||||||| |||| |||||:          |||         || :| | |: :||
Db     127 YSGILLLACISVDRYLAIVHATR----------TLTQKRHLVKFICLGIWALSLILSLPF 176

Qy     234 FIF---LSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           |:|    | ::   :      :|  :  |  ||:|    ||:|||||| :||   |  |
Db     177 FLFRQVFSPNNSSPVCYEDLGHNTAK-WRMVLRILPHTFGFILPLLVMLFCYGFTLRTLF 235

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           :   :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |
Db     236 QAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTHVIQETCQRRNDIDRALDAT 295

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSS 403
             ||::| ||||::|||:|  ||     :|   |  ::  | |   :|   ||
Db     296 EILGFLHSCLNPIIYAFIGQNFRNGFLKMLAARGLISKEFLTRHRVTSYTSSS 348


RESULT 8
A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53752
R;Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarro
J. Biol. Chem. 269, 12391-12394, 1994
A;Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.
A;Reference number: A53752; MUID:94230294
A;Accession: A53752
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-358 <PRA>
A;Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             28.6%;  Score 615;  DB 2;  Length 358;
  Best Local Similarity   39.7%;  Pred. No. 1.5e-46;
  Matches  141;  Conservative   55;  Mismatches  139;  Indels   20;  Gaps    6;

Qy      68 ENFS--------SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNG 119
           ||:|        |:| |  :   :   | ||  : ||  :   :   | |:||| ||||
Db       7 ENYSYEDFFGDFSNYSYSTDLPPTLLDSAPCRSE-SLETNSYVVLITYILVFLLSLLGNS 65

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  |:|  |:  | || :||:||:|| |   |||:||      | ||: ||||   :
Db      66 LVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSLVKE 125

Qy     180 INFYAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFL 237
           :|||:| ||||||| |||| |||||:  : :|     |   ||::||: |: :||  :|
Db     126 VNFYSGILLLACISVDRYLAIVHATRTMIQKR---HLVKFICLSMWGVSLILSLPILLFR 182

Qy     238 SAHHDERLNATHCQY----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSR 293
           :|      |::   |    |    |  ||:|    ||:|||||| :||   |  |  :
Db     183 NAIFPP--NSSPVCYEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAH 240

Qy     294 GQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGL 353
             :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  |
Db     241 MGQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRALDATEIL 300

Qy     354 GYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           |::| ||||::|||:| |||  :  :|   |  ::  | ::   |   ||   ||
Db     301 GFLHSCLNPIIYAFIGQKFRYGLLKILAAHGLISKEFLAKESRPSFVASSSGNTS 355


RESULT 9
A39445
interleukin-8 receptor type A - human
N;Alternate names: interleukin-8 receptor, high-affinity
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: I37449; I38710; I38711; A39445
R;Mollereau, C.; Muscatelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A;Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 r
A;Reference number: I37449; MUID:93252387
A;Accession: I37449
A;Molecule type: DNA
A;Residues: 1-350 <RES>
A;Cross-references: EMBL:X65858; NID:g312046; PIDN:CAA46688.1; PID:g312047
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter function for human inter
A;Reference number: I37898; MUID:95014476
A;Accession: I38710
A;Molecule type: DNA
A;Residues: 1-350 <RE2>
A;Cross-references: EMBL:U11870; NID:g511804; PIDN:AAA64378.1; PID:g511805
A;Accession: I38711
A;Molecule type: mRNA
A;Residues: 1-16 <RE3>
A;Cross-references: EMBL:U11871; NID:g511806; PIDN:AAA64379.1; PID:g733002
R;Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A;Title: Structure and functional expression of a human interleukin-8 receptor.
A;Reference number: A39445; MUID:91368199
A;Accession: A39445
A;Molecule type: mRNA
A;Residues: 1-275,'T',277-350 <HOL>
A;Cross-references: GB:M68932; NID:g186369; PIDN:AAA59159.1; PID:g186370
C;Genetics:
A;Gene: GDB:IL8RA
A;Cross-references: GDB:135039; OMIM:146929
A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

  Query Match             28.2%;  Score 606.5;  DB 2;  Length 350;
  Best Local Similarity   39.7%;  Pred. No. 8.4e-46;
  Matches  135;  Conservative   50;  Mismatches  124;  Indels   31;  Gaps    5;

Qy      88 PPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH 141
           ||  :|:|         ::  :   |:|:||| ||||  |  |:|  |   |  || :||:
Db      21 PPADEDYSPCMLETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLN 80

Qy     142 LAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIV 201
           ||:|| |  ||||:||      |:||: |||   |  :|||:| |||||| |||| ||
Db      81 LALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIV 140

Qy     202 HATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQY 252
           |||:          |||         ||  ||| :  :|| |:|  |:|    |::   |
Db     141 HATR----------TLTQKRHLVKFVCLGCWGLSMNLSLPFFLFRQAYHPN--NSSPVCY 188

Qy     253 ----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
               |     |  ||:|    ||::|| || :||   |  |  :   :: ||||::  ||
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Db    189 EVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVV 248

Qy    309 VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
          : | ||| ||:||:| | ||    :  :| | : :  |   |  ||:::| ||||::|||:
Db    249 LIFLLCWLPYNLVLLADTLMRTQVIQESCERRNNIGRALDATEILGFLHSCLNPIIYAFI 308

Qy    369 GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
          |  ||     :|   |  ::  | |   :|   || : :|
Db    309 GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348


RESULT 10
S42096
interleukin-8 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C;Accession: S42096
R;Gobl, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.
submitted to the EMBL Data Library, February 1994
A;Description: Molecular cloning of the rat IL8 receptor.
A;Reference number: S42096
A;Accession: S42096
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-356 <GOB>
A;Cross-references: EMBL:X77797
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

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Qy     67 LENFSS----SYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVA 122
          ||:| |    ||::  :   :   : |||   :|: :|  :  :| |: || ||:||  |
Db     11 LEDFFSGDIDSYNFSSDPPFTLSDAAPCP-SANLDINRYAVVVIYVLVTLLSLVGNSLVM 69

Qy    123 AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
           |:|  |:  | || :||:||:||    ||||:||      |:||| ||||   |  | |
Db     70 LVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQEITF 129

Qy    183 YAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
          |:  ||||||| |||| |||||   : :|     |   |: :| | |: :|| || |
Db    130 YSSVLLLACISMDRYLAIVHATSTLIQKR---HLVKFVCITMWFLSLVLSLPIFI-LRTT 185

Qy    241 HDERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRG 294
              :   | |   :|       |  ||:|    |||||||:| :||   |  |  :
Db    186 VKANPSTVVCYEN---IGNNTSKWRVVLRILPQTYGFLLPLLIMLFCYGFTLRTLFKAHM 242

Qy    295 QRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLG 354
           :: ||||::  ||: | ||| ||::|:  | ||    :   | |:: :: |  :   ||
Db    243 GQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINKASEI---LG 299

Qy    355 YMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
          ::| ||||::|||:| |||  :  ::   |  ::  | ::   |   || : ||
Db    300 FLHSCLNPIIYAFIGQKFRHGLLKIMANYGLVSKEFLAKEGRPSFVGSSSANTS 353


RESULT 11
B55735
lymphocyte-specific G protein-coupled receptor EBI1 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically tra
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

  Query Match             27.2%;  Score 586;  DB 2;  Length 378;
  Best Local Similarity   38.4%;  Pred. No. 5.9e-44;
  Matches  133;  Conservative   62;  Mismatches  139;  Indels   12;  Gaps    7;

Qy     75 DY-GENES-DSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTAL 132
          || |:| : |       | :    ||   ||| :||::  :||||||  |    :  :
Db     31 DYIGDNTTVDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLTYIYFKRLK 90

Qy    133 SSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACI 192
          : |||:||:||||| | :|||| ||  ||  ||||   ||:  |:: ::|::| ||| ||
Db     91 TMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFSGMLLLLCI 150

Qy    193 SFDRYLNIVHATQLYRRGPPARV----TLTCLAVWGLCLLFALPDFIFLSAHHDERLNAT 248
          | |||: || |   :|    |||     |:|: :| |  : ::|: ::          |
Db    151 SIDRYVAIVQAVSAHRH--RARVLLISKLSCVGIWILATVLSIPELLYSDLQRSSSEQAM 208

Qy    249 HCQYNFPQV-GRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVV 307
           |       |      ::| |:| |||:||| |::||   |:  || :|   | :|:::: |
Db    209 RCSLITEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNFERNKAIKVIIAV 268

Qy    308 VVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAF 367
          || | :   ||: |||   : :   :  |    ::::|  ||  |  : ||:|| ||||
Db    269 VVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLACVRCCVNPFLYAF 328

Qy    368 VGVKFRERMWMLLLRLGCPNQRGLQRQPSSSR--RDSSWSETSEAS 411
          :|||||  :: |   ||| :|  | || || |  | || |  :| :
Db    329 IGVKFRNDLFKLFKDLGCLSQEQL-RQWSSCRHIRRSSMSVEAETT 373


RESULT 12
G00048
fusin (LESTRA) - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 26-Aug-1999
C;Accession: G00048
R;Tatsumi, M.
submitted to GenBank, July 1996
A;Reference number: H00048
A;Accession: G00048
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <TAT>
A;Cross-references: GB:D86579; NID:g1468948; PID:g1468949
C;Superfamily: vertebrate rhodopsin

  Query Match             27.1%;  Score 582.5;  DB 2;  Length 352;
  Best Local Similarity   35.4%;  Pred. No. 1.1e-43;
  Matches  123;  Conservative   70;  Mismatches  137;  Indels   17;  Gaps    5;

Qy     68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
          :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db     10 DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 65

Qy    128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
          ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db     66 QKKLRSMTDKYRLHLSVADLLYVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125
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Qy    188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLS-AHHDERLN 246
          :|| || |||| |||||   |        :  : ||   ||  :||||| | :  |:|
Db    126 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEADDRY- 184

Qy    247 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |
Db    185 --ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 242

Qy    306 VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
          ::::||  || ||:: : :|  : |  : : |  |: |    |:|  ||: ||||||:||
Db    243 ILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALGFFHCCLNPILY 302

Qy    366 AFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
          ||:| ||:      |        |::    :||     |:    ||:
Db    303 AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 349


RESULT 13
A45747
neuropeptide Y/peptide YY receptor Y3 - human
N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LESTR; re
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
C;Accession: A45747; A53103; I53006; I59444; I69203; S32761
R;Federsppiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lewi
Genomics 16, 707-712, 1993
A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a pu
A;Reference number: A45747; MUID:93315164
A;Accession: A45747
A;Molecule type: mRNA
A;Residues: 1-352 <FED>
A;Cross-references: GB:M99293; NID:g292516; PIDN:AAA16617.1; PID:g292517
R;Loetscher, M.; Geiser, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.
J. Biol. Chem. 269, 232-237, 1994
A;Title: Cloning of a human seven-transmembrane domain receptor, LESTR, that is highly e
A;Reference number: A53103; MUID:94103215
A;Accession: A53103
A;Molecule type: mRNA
A;Residues: 1-352 <LOE>
A;Cross-references: EMBL:X71635; NID:g297099; PIDN:CAA50641.1; PID:g297100
R;Herzog, H.; Hort, Y.J.; Shine, J.; Selbie, L.A.
DNA Cell Biol. 12, 465-471, 1993
A;Title: Molecular cloning, characterization, and localization of the human homolog to t
A;Reference number: I53006; MUID:93319629
A;Accession: I53006
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <HER>
A;Cross-references: GB:L06797; NID:g414929; PIDN:AAA03209.1; PID:g414928
R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salon, J.; Lar
Regul. Pept. 47, 247-258, 1993
A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human homolo
A;Reference number: I59444; MUID:94052833
A;Accession: I59444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RE2>
A;Cross-references: GB:L01639; NID:g189313; PIDN:AAA16594.1; PID:g189314
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A;Reference number: I54751; MUID:94092629
A;Accession: I69203
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-352 <RES>
A;Cross-references: GB:D10924; NID:g219868; PIDN:BAA01722.1; PID:g219869
C;Genetics:
A;Gene: GDB:NPY3R; NPYY3
A;Cross-references: GDB:230002; OMIM:162643
A;Map position: 2q21-2q21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             26.8%;  Score 576.5;  DB 2;  Length 352;
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  Matches  121;  Conservative   70;  Mismatches  140;  Indels   15;  Gaps    4;

Qy     68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
          :|::     |: :|       || :: : ||:: ||| :||::|| |::||| |  |:
Db     10 DNYTEEMGSGDYDS----MKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 65

Qy    128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
          ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db     66 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 125

Qy    188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
          :|| || |||| |||||   |        :  : ||   ||  :|||||  |:  |  :
Db    126 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 183

Qy    248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
            |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db    184 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 243

Qy    307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
          :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db    244 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 303

Qy    367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
          |:| ||:      |        |::    :||     |:    ||:
Db    304 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 349


RESULT 14
A48921
interleukin-8 receptor type B - mouse
N;Alternate names: G-protein coupled receptor Gpcr16
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: A48921; A53677; I49348; I55421; H48909; I53774
R;Cerretti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilber
Genomics 18, 410-413, 1993
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near th
A;Reference number: A48921; MUID:94117014
A;Accession: A48921
A;Molecule type: DNA
A;Residues: 1-359 <CER>
A;Cross-references: GB:L23637; NID:g435093; PIDN:AAA39305.1; PID:g435094
R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.
J. Biol. Chem. 269, 18263-18266, 1994
A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity bindin
A;Reference number: A53677; MUID:94308043
A;Accession: A53677
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-359 <SUZ>
A;Cross-references: GB:L26549
A;Note: sequence extracted from NCBI backbone (NCBIP:149812)
R;Lee, J.; Cacalano, G.; Camerato, T.; Toy, K.; Moore, M.W.; Wood, W.I.
J. Immunol. 155, 2158-2164, 1995
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.
A;Reference number: I49348; MUID:95363183
A;Accession: I49348
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RES>
A;Cross-references: EMBL:U31207; NID:g950174; PIDN:AAC52239.1; PID:g950175
R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.
J. Biol. Chem. 269, 29355-29358, 1994
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expressi
A;Reference number: I55421; MUID:95050766
A;Accession: I55421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-359 <RE2>
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A;Cross-references: GB:L13239; NID:g293665; PIDN:AAA62109.1; PID:g293666
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G
Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A;Reference number: A48909; MUID:94116980
A;Accession: H48909
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 145-258 <WIL>
A;Cross-references: GB:L20337; NID:g438800; PIDN:AAA16853.1; PID:g438801
R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.
Gene 142, 297-300, 1994
A;Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.
A;Reference number: I53774; MUID:94252584
A;Accession: I53774
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <RE3>
A;Cross-references: GB:D17630; NID:g493671; PIDN:BAA04536.1; PID:g493672
C;Genetics:
A;Gene: Il8rb
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F;49-74/Domain: transmembrane #status predicted <TM1>
F;84-106/Domain: transmembrane #status predicted <TM2>
F;120-141/Domain: transmembrane #status predicted <TM3>
F;163-182/Domain: transmembrane #status predicted <TM4>
F;213-234/Domain: transmembrane #status predicted <TM5>
F;251-271/Domain: transmembrane #status predicted <TM6>
F;308-328/Domain: transmembrane #status predicted <TM7>

  Query Match             26.6%;  Score 573;  DB 2;  Length 359;
  Best Local Similarity   36.7%;  Pred. No. 7.8e-43;
  Matches  130;  Conservative   59;  Mismatches  145;  Indels   20;  Gaps    7;

Qy      67 LENFSSS----YDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVA 122
           :|:| |     ::|          : ||  : :|  :   :  :| |: || |:||  |
Db      11 IEDFFSGDLDIFNYSSGMPSILPDAVPCHSE-NLEINSYAVVVIYVLVTLLSLVGNSLVM 69

Qy     123 AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
            |:|  |:  | || :||:||:||    ||||:||      | ||| |||:   :  : |
Db      70 LVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWTFGSTLCKIFSYVKEVTF 129

Qy     183 YAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           |:  ||||||| |||| |||||   : :|     |   |:|:| | :: |||  : |
Db     130 YSSVLLLACISMDRYLAIVHATSTLIQKR---HLVKFVCIAMWLLSVILALP-ILILRNP 185

Qy     241 HDERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRG 294
               |:   |   :  ||       |  ||:|    |||:|||:| :||   |  |  :
Db     186 VKVNLSTLVC---YEDVGNNTSRLRVVLRILPQTFGFLVPLLIMLFCYGFTLRTLFKAHM 242

Qy     295 QRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLG 354
            :: ||||::  ||: | ||| ||:||:  | ||    :   | |   :| | : |  ||
Db     243 GQKHRAMRVIFAVVLVFLLCWLPYNLVLFTDTLMRTKLIKETCERRDDIDKALNATEILG 302

Qy     355 YMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           ::| ||||::|||:| |||  :  ::   |  ::  | ::   |   || : ||
Db     303 FLHSCLNPIIYAFIGQKFRHGLLKIMATYGLVSKEFLAKEGRPSFVSSSSANTS 356


RESULT 15
S28787
neuropeptide Y/peptide YY receptor Y3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
C;Accession: S28787
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
Mol. Pharmacol. 40, 869-875, 1991
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.
A;Reference number: S28787; MUID:92100053
A;Accession: S28787
A;Molecule type: mRNA
A;Residues: 1-353 <RIM>
A;Cross-references: EMBL:M86739
C;Superfamily: vertebrate rhodopsin
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

  Query Match             26.5%;  Score 571;  DB 2;  Length 353;
  Best Local Similarity   35.7%;  Pred. No. 1.2e-42;
  Matches  124;  Conservative   64;  Mismatches  143;  Indels   16;  Gaps    6;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::   | |  : ||     || :: : :|:| ||| :||::|| |::||| |  |:
Db      10 DNYTED-DLGSGDYDS--MKEPCFREENAHFNRIFLPTVYSIIFLTGIVGNGLVILVMGY 66

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | ||||| |||||   | ||  |||    :: :| |:  |
Db      67 QKKLRSMTDKYRLHLSVADLLFVLTLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 126

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHH-DERLN 246
           :|| || |||| |||||   :        :  : ||   :|  :|| ||      |||
Db     127 ILAFISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWLPAVLLTIPDLIFADIKEVDERY- 185

Qy     247 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
              |   :|  :      :   :| | ||| :|:  ||  |:: |  |:| :: :|::  |
Db     186 --ICDRFYPSDLWLVVFQFQHIVVGLLLPGIVILSCYCIIISKLSHSKGYQKRKALKTTV 243

Qy     306 VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
           :::: |  || ||:: : :|  : |  : : |  || |    |:|  | : ||||||:||
Db     244 ILILTFFACWLPYYIGISIDSFILLEIIQQGCEFESTVHKWISITEALAFFHCCLNPILY 303

Qy     366 AFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           ||:| ||:       |        |::    :||     |:    ||:
Db     304 AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 350


Search completed: November 2, 2002, 12:08:01
Job time : 46 secs
```

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 06:53:33 ; Search time 26 Seconds
(without alignments)
618.024 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1891	87.9	368	1	CCR3_HUMAN	P49682 homo sapien
2	1626.5	75.6	367	1	CCR3_MOUSE	O88410 mus musculu
3	641	29.8	374	1	CCR5_RAT	P34997 rattus norv
4	640	29.8	374	1	CCR5_MOUSE	Q04683 mus musculu
5	635	29.5	372	1	CCR5_HUMAN	P32302 homo sapien
6	633	29.4	360	1	IL8B_HUMAN	P25025 homo sapien
7	629.5	29.3	353	1	IL8B_MACMU	Q28519 macaca mula
8	622	28.9	353	1	IL8B_PANTR	Q28807 pan troglod
9	615.5	28.6	355	1	IL8A_RABIT	P21109 oryctolagus
10	615	28.6	358	1	IL8B_RABIT	P35344 oryctolagus
11	614	28.5	353	1	IL8B_GORGO	Q28422 gorilla gor
12	612.5	28.5	350	1	IL8A_GORGO	P55919 gorilla gor
13	606	28.2	360	1	IL8B_BOVIN	Q28003 bos taurus
14	605.5	28.1	350	1	IL8A_HUMAN	P25024 homo sapien
15	605	28.1	359	1	IL8B_RAT	P35407 rattus norv
16	600	27.9	350	1	IL8A_PANTR	P55920 pan troglod
17	590	27.4	356	1	IL8B_CANFA	O97571 canis famil
18	586	27.2	378	1	CKR7_HUMAN	P32248 homo sapien
19	584	27.2	359	1	CCR4_MOUSE	P70658 m c-x-c che
20	582.5	27.1	352	1	CCR4_MACFA	Q28474 macaca fasc
21	577.5	26.8	352	1	CCR4_PAPAN	P56491 papio anubi
22	577	26.8	353	1	CCR4_FELCA	P56498 felis silve
23	576.5	26.8	352	1	CCR4_HUMAN	P30991 homo sapien
24	573	26.6	359	1	IL8B_MOUSE	P35343 mus musculu
25	571	26.5	353	1	CCR4_BOVIN	P25930 bos taurus
26	568.5	26.4	352	1	CCR4_CERTO	O62747 cercocebus
27	567.5	26.4	352	1	CCR4_MACMU	P79394 macaca mula
28	567.5	26.4	378	1	CKR7_MOUSE	P47774 mus musculu
29	566.5	26.3	378	1	CKD6_MOUSE	O08707 mus musculu
30	565.5	26.3	349	1	CCR4_RAT	O08565 rattus norv
31	563.5	26.2	374	1	CKR6_HUMAN	P51684 homo sapien
32	559	26.0	382	1	CKD6_RAT	O09027 rattus norv
33	552.5	25.7	349	1	IL8A_RAT	P70612 rattus norv
34	551.5	25.6	360	1	CKR4_HUMAN	P51679 homo sapien
35	549.5	25.5	362	1	CKRA_MOUSE	Q9j121 mus musculu
36	548.5	25.5	384	1	CKD6_HUMAN	O00590 homo sapien
37	548	25.5	360	1	CKR4_MOUSE	P51680 mus musculu
38	547.5	25.5	367	1	CKR6_MOUSE	O54689 mus musculu
39	539.5	25.1	362	1	CKRA_HUMAN	P46092 homo sapien
40	535	24.9	373	1	CKR2_RAT	O55193 rattus norv
41	534.5	24.8	374	1	CKR2_HUMAN	P41597 homo sapien
42	528	24.5	360	1	CKR2_MACMU	O18793 macaca mula
43	528	24.5	373	1	CKR2_MOUSE	P51683 mus musculu
44	520	24.2	352	1	CKR5_MACMU	P79436 macaca mula
45	519.5	24.2	352	1	CKR5_CERAE	P56493 cercopithec

ALIGNMENTS

RESULT 1
CCR3_HUMAN
ID CCR3_HUMAN STANDARD; PRT; 368 AA.
AC P49682; O15185;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXC-R3) (CXCR-3) (CKR-L2) (CD183
DE antigen).
GN CXCR3 OR GPR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,
RA Clark-Lewis I., Baggiolini M., Moser B.;
RT "Chemokine receptor specific for IP10 and mig: structure, function,
RT and expression in activated T-lymphocytes.";
RL J. Exp. Med. 184:963-969(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Gutierrez J., Varona R., Zaballos A., Lind P., Marquez G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 5-368 FROM N.A.
RX MEDLINE=96115583; PubMed=8666380;
RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saldivia V.R.,
RA Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA O'Dowd B.F., Docherty J.M.;
RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT Y, and somatostatin receptors.";
RL Genomics 29:335-344(1995).
RN [4]
RP LIGAND BINDING.
RC TISSUE=Fetal astrocytes;
RX MEDLINE=98290735; PubMed=9625760;
RA Cole K.E., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
RA Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
RA Neote K.;
RT "Interferon-inducible T cell alpha chemoattractant (I-TAC): A novel
RT non-ELR CXC chemokine with potent activity on activated T cells
RT through selective high affinity binding to CXCR3.";
RL J. Exp. Med. 187:2009-2021(1998).
CC -!- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD183 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/650534941_g.htm".
CC ---
CC

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CC   ---------------------------------------------------------------------------
DR   EMBL; X95876; CAA65126.1; -.
DR   EMBL; Z79783; CAB02143.1; ALT_INIT.
DR   EMBL; U32674; AAC50505.1; -.
DR   GCRDb; GCR_1341; -.
DR   GCRDb; GCR_1972; -.
DR   MIM; 600894; -.
DR   InterPro; IPR004070; CXCchemok_receptor3.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01532; CXCCHMKINER3.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Antigen.
FT   DOMAIN        1     53       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     54     80       1 (POTENTIAL).
FT   DOMAIN       81     89       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     90    110       2 (POTENTIAL).
FT   DOMAIN      111    125       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    126    147       3 (POTENTIAL).
FT   DOMAIN      148    169       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    170    189       4 (POTENTIAL).
FT   DOMAIN      190    212       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    213    233       5 (POTENTIAL).
FT   DOMAIN      234    255       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    256    277       6 (POTENTIAL).
FT   DOMAIN      278    298       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    299    321       7 (POTENTIAL).
FT   DOMAIN      322    368       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    203       BY SIMILARITY.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     75     75       A -> R (IN REF. 2).
SQ   SEQUENCE   368 AA;  40659 MW;  F08A3B44B2BBAD04 CRC64;

  Query Match             87.9%;  Score 1891;  DB 1;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-123;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368
```

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RESULT 2
CCR3_MOUSE
ID   CCR3_MOUSE     STANDARD;      PRT;   367 AA.
AC   O88410;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-X-C chemokine receptor type 3 (CXC-R3) (CXCR-3).
GN   CXCR3 OR CMKAR3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98318636; PubMed=9653165;
RA   Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
RA   Jenkins N.A., Hedrick J., Zlotnik A.;
RT   "The CC chemokine 6Ckine binds the CXC chemokine receptor CXCR3.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
CC   -!- FUNCTION: RECEPTOR FOR SCYB9/MIG, SCYB10/INP10 AND SCYB11/ITAC (BY
CC       SIMILARITY). BINDS TO SCYA21.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF045146; AAC40163.1; -.
DR   MGD; MGI:1277207; Cmkar3.
DR   InterPro; IPR004070; CXCchemok_receptor3.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01532; CXCCHMKINER3.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     79       1 (POTENTIAL).
FT   DOMAIN       80     88       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     89    109       2 (POTENTIAL).
FT   DOMAIN      110    124       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    125    146       3 (POTENTIAL).
FT   DOMAIN      147    168       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    169    188       4 (POTENTIAL).
FT   DOMAIN      189    211       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    212    232       5 (POTENTIAL).
FT   DOMAIN      233    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    276       6 (POTENTIAL).
FT   DOMAIN      277    297       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    298    320       7 (POTENTIAL).
FT   DOMAIN      321    367       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    123    202       BY SIMILARITY.
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   367 AA;  41016 MW;  029FBB778E3CD4EA CRC64;

  Query Match             75.6%;  Score 1626.5;  DB 1;  Length 367;
  Best Local Similarity   86.0%;  Pred. No. 2.8e-105;
  Matches  314;  Conservative   22;  Mismatches   28;  Indels    1;  Gaps    1;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||: |||: :: | |||| :| |||||||||    ||||||||||||| |||||||||
Db       4 EVSERQVLDASDFAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL 62

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
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          ||||||||||||||||||:||||||||||||||||| |||||||||||||||||||| ||
Db      63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           |||||||||||||||| ||||||||||:||||||:||| |  || |||: |||||||||
Db     123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFA 182

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           |||||:|||::|:||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 242

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||| |||||||||| |||:|||||||||||||||:| |||||||:| ||||||||
Db     243 VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRKSHVDVAKSVT 302

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||:|||||||||||||||||||:|||| |||  :||| |||||||||:||||||:||
Db     303 SGMGYMHCCLNPLLYAFVGVKFREKMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy     411 SYSGL 415
           || ||
Db     363 SYLGL 367


RESULT 3
CCR5_RAT
ID   CCR5_RAT       STANDARD;      PRT;   374 AA.
AC   P34997;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma
DE   receptor 1 homolog) (Neurolymphatic receptor) (NLR).
GN   BLR1 OR CXCR5.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=93238948; PubMed=8386678;
RA   Kouba M., Vanetti M., Wang X., Schaefer M., Hoellt V.;
RT   "Cloning of a novel putative G-protein-coupled receptor (NLR) which
RT   is expressed in neuronal and lymphatic tissue.";
RL   FEBS Lett. 321:173-178(1993).
CC   -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC       CHEMOATTRACTANT (BLC) (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X71463; CAA50582.1; -.
DR   PIR; S32785; S32785.
DR   GCRDb; GCR_0648; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
FT   DOMAIN       1     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     58    78       1 (POTENTIAL).
FT   DOMAIN       79    90       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     91    111      2 (POTENTIAL).
FT   DOMAIN       112   126      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     127   147      3 (POTENTIAL).
FT   DOMAIN       148   169      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     170   190      4 (POTENTIAL).
FT   DOMAIN       191   221      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     222   242      5 (POTENTIAL).
FT   DOMAIN       243   261      CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     262   282      6 (POTENTIAL).
FT   DOMAIN       283   306      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     307   327      7 (POTENTIAL).
FT   DOMAIN       328   374      CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      28    28      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     198   198      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     124   204      POTENTIAL.
SQ   SEQUENCE   374 AA;  42012 MW;  D87A3AC816207319 CRC64;

  Query Match             29.8%;  Score 641;  DB 1;  Length 374;
  Best Local Similarity   41.7%;  Pred. No. 2.1e-37;
  Matches  146;  Conservative   50;  Mismatches  140;  Indels   14;  Gaps    6;

Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           :|:| :    :|  | |          :|   |:|  |||:||||::||  |  :|   |
Db      26 YSNSTEIPLQDSIFCSTE---EGPLLTSFKTIFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
           |||:||| |||||| |||  ||    : :| || |: |||   ||  ||||  :|||
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLL 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIF---LSAHHDERLN 246
           |||: |||| ||||   |||     : :||  :|    |||||: :|   :  |::| |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCSTIWLAGFLFALPELLFAKVVQPHNNESL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
           | ::      |    | | |    |||||:||||:|| ::  ||   |  :| :|:
Db     202 -PQCIFSQENEAETRAWFASRFLYHTGGFLLPMLVMAWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFLLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |     | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPGWRKSSLSESENAT 369


RESULT 4
CCR5_MOUSE
ID   CCR5_MOUSE     STANDARD;      PRT;   374 AA.
AC   Q04683;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma
DE   receptor 1 homolog).
GN   BLR1 OR CXCR5 OR GPCR6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=Liver;
RX   MEDLINE=94009211; PubMed=8405054;
RA   Kaiser E., Foerster R., Wolf I., Epensperger C., Kuehl W.M., Lipp M.;
RT   "The G protein-coupled receptor BLR1 is involved in murine B cell
RT   differentiation and is also expressed in neuronal tissues.";
RL   Eur. J. Immunol. 23:2532-2539(1993).
RN   [2]
RP   SEQUENCE OF 151-269 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=94116980; PubMed=8288218;
RA   Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
RA   Copeland N.G., Jenkins N.A.;
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RT   "Identification, chromosomal location, and genome organization of
RT   mammalian G-protein-coupled receptors.";
RL   Genomics 18:175-184(1993).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=97133211; PubMed=8978608;
RA   Foerster R., Mattis A.E., Kremmer E., Wolf E., Brem G., Lipp M.;
RT   "A putative chemokine receptor, BLR1, directs B cell migration to
RT   defined lymphoid organs and specific anatomic compartments of the
RT   spleen.";
RL   Cell 87:1037-1047(1996).
RN   [4]
RP   LIGAND BINDING.
RX   MEDLINE=98146056; PubMed=9486651;
RA   Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G.,
RA   Williams L.T.;
RT   "A B-cell-homing chemokine made in lymphoid follicles activates
RT   Burkitt's lymphoma receptor-1.";
RL   Nature 391:799-803(1998).
CC   -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC       CHEMOATTRACTANT (BLC). INVOLVED IN B-CELL MIGRATION INTO B-CELL
CC       FOLLICLES OF SPLEEN AND PEYER'S PATCHES, BUT NOT IN THOSE OF
CC       MESENTRIC OR PERIPHERAL LYMPH NODES.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY IN SPLEEN, IN RESTING B-CELLS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X71788; CAA50673.1; -.
DR   EMBL; L20332; AAA16852.1; -.
DR   PIR; S42628; S42628.
DR   GCRDb; GCR_0809; -.
DR   GCRDb; GCR_0832; -.
DR   MGD; MGI:103567; Blr1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
FT   DOMAIN        1     57       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     58     78       1 (POTENTIAL).
FT   DOMAIN       79     90       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     91    111       2 (POTENTIAL).
FT   DOMAIN      112    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    169       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    170    190       4 (POTENTIAL).
FT   DOMAIN      191    221       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    222    242       5 (POTENTIAL).
FT   DOMAIN      243    261       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    262    282       6 (POTENTIAL).
FT   DOMAIN      283    306       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    307    327       7 (POTENTIAL).
FT   DOMAIN      328    374       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    198    198       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    124    204       POTENTIAL.
SQ   SEQUENCE   374 AA;  42100 MW;  385258420C1EDE30 CRC64;

  Query Match             29.8%;  Score 640;  DB 1;  Length 374;
  Best Local Similarity   40.9%;  Pred. No. 2.4e-37;
  Matches  143;  Conservative   54;  Mismatches  139;  Indels   14;  Gaps    6;

Qy      70 FSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           :|:| :    :|: | |          :|   |:|  |||:||||::||  |  :|   |

Db      26 YSNSTEIPLQDSNFCST---VEGPLLTSFKAVFMPVAYSLIFLLGMMGNILVLVILERHR 82

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
              |||:||| |||||| |||  ||    : :| || |: |||   ||  ||||  :||:
Db      83 HTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHKINFYCSSLLV 142

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA---HHDERLN 246
           |||: |||| ||||   |||     : :|| |:|    |||||: :|      |::: |
Db     143 ACIAVDRYLAIVHAVHAYRRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSL- 201

Qy     247 ATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVLL-VSRGQRRLRAM 301
           | ::      |       | |  : ||||:||| :|| ::  ||   |  :| :|:
Db     202 -PQCTFSQENEAETRAWFTSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAV 260

Qy     302 RLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLN 361
           |: ::|   | |||:|||:|: :| |  | |:  :|     : || ::   ||  |||||
Db     261 RVAILVTSIFFLCWSPYHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLN 320

Qy     362 PLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |:|| | |||||  :  || :|||     |  |   : | || ||:  |:
Db     321 PMLYTFAGVKFRSDLSRLLTKLGCAGPASL-CQLFPNWRKSSLSESENAT 369


RESULT 5
CCR5_HUMAN
ID   CCR5_HUMAN     STANDARD;      PRT;   372 AA.
AC   P32302; Q14811;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-X-C chemokine receptor type 5 (CXC-R5) (CXCR-5) (Burkitt'S lymphoma
DE   receptor 1) (Monocyte-derived receptor 15) (MDR15).
GN   BLR1 OR CXCR5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG FORM).
RC   TISSUE=Lymphocytes;
RX   MEDLINE=93049615; PubMed=1425907;
RA   Dobner T., Wolf I., Emrich T., Lipp M.;
RT   "Differentiation-specific expression of a novel G protein-coupled
RT   receptor from Burkitt's lymphoma.";
RL   Eur. J. Immunol. 22:2795-2799(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (SHORT FORM).
RC   TISSUE=Blood;
RX   MEDLINE=95366951; PubMed=7639692;
RA   Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;
RT   "Sequence variation of a novel heptahelical leucocyte receptor
RT   through alternative transcript formation.";
RL   Biochem. J. 309:773-779(1995).
RN   [3]
RP   LIGAND BINDING.
RX   MEDLINE=98130629; PubMed=9463416;
RA   Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,
RA   Baggiolini M., Moser B.;
RT   "B cell-attracting chemokine 1, a human CXC chemokine expressed in
RT   lymphoid tissues, selectively attracts B lymphocytes via
RT   BLR1/CXCR5.";
RL   J. Exp. Med. 187:655-660(1998).
CC   -!- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO BLC. BLR1 EXERTS
CC       POSSIBLY A REGULATORY FUNCTION IN BURKITT LYMPHOMA (BL)
CC       LYMPHOMAGENESIS AND/OR B-CELL DIFFERENTIATION. IT IS A POTENTIAL
CC       CANDIDATE FOR CELL-CELL INTERACTION, AND ACTIVATION OF MATURE B-
CC       LYMPHOCYTES IN LYMPHATIC TISSUES.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSION IN MATURE B-CELLS AND BURKITT
CC       LYMPHOMA CELLS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC   ----------------------------------------------------------------------
DR   EMBL; X68149; CAA48252.1; -.
DR   EMBL; X68829; CAA48723.1; -.
DR   PIR; S26667; S26667.
DR   GCRDb; GCR_0453; -.
DR   GCRDb; GCR_2072; -.
DR   GCRDb; GCR_2612; -.
DR   MIM; 601613; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell;
KW   Alternative splicing; Polymorphism.
FT   DOMAIN        1     55       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     56     76       1 (POTENTIAL).
FT   DOMAIN       77     88       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     89    109       2 (POTENTIAL).
FT   DOMAIN      110    124       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    125    145       3 (POTENTIAL).
FT   DOMAIN      146    167       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    168    188       4 (POTENTIAL).
FT   DOMAIN      189    219       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    220    240       5 (POTENTIAL).
FT   DOMAIN      241    259       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    260    280       6 (POTENTIAL).
FT   DOMAIN      281    304       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    305    325       7 (POTENTIAL).
FT   DOMAIN      326    372       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    196    196       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    122    202       POTENTIAL.
FT   VARSPLIC      1     45       MISSING (IN SHORT ISOFORM).
FT   VARIANT     344    344       G -> S (IN DBSNP:665648).
FT                                /FTId=VAR_011838.
SQ   SEQUENCE   372 AA;  41955 MW;  6DF84C839492ACCF CRC64;

  Query Match             29.5%;  Score 635;  DB 1;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 5.3e-37;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |    :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |   |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||      : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::       |      | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|   | |||:|||:|: :| |  | |:   |     : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | |||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367
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RESULT 6
IL8B_HUMAN
ID   IL8B_HUMAN     STANDARD;      PRT;   360 AA.
AC   P25025;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
DE   receptor) (IL-8 receptor type 2) (CDw128b).
GN   IL8RB OR CXCR2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91368200; PubMed=1891716;
RA   Murphy P.M., Tiffany H.L.;
RT   "Cloning of complementary DNA encoding a functional human
RT   interleukin-8 receptor.";
RL   Science 253:1280-1283(1991).
RN   [2]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=93205012; PubMed=8384312;
RA   Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA   Beckmann M.P.;
RT   "Molecular characterization of receptors for human interleukin-8,
RT   GRO/melanoma growth-stimulatory activity and neutrophil activating
RT   peptide-2.";
RL   Mol. Immunol. 30:359-367(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94209273; PubMed=7512557;
RA   Sprenger H., Lloyd A.R., Lautens L.L., Bonner T.I., Kelvin D.J.;
RT   "Structure, genomic organization, and expression of the human
RT   interleukin-8 receptor B gene.";
RL   J. Biol. Chem. 269:11065-11072(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=95014476; PubMed=7929358;
RA   Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT   "Comparison of the genomic organization and promoter function for
RT   human interleukin-8 receptors A and B.";
RL   J. Biol. Chem. 269:26381-26389(1994).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=92355587; PubMed=1379593;
RA   Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT   "Characterization of two high affinity human interleukin-8
RT   receptors.";
RL   J. Biol. Chem. 267:16283-16287(1992).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw128b entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128b.htm".
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CC   ----------------------------------------------------------------------
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DR   EMBL; M73969; AAA83148.1; -.
DR   EMBL; M94582; AAA36108.1; -.
DR   EMBL; M99412; AAC14460.1; -.
DR   EMBL; L19593; AAB59437.1; -.
DR   EMBL; U11869; AAB60656.1; -.
DR   PIR; A39446; A39446.
DR   PIR; A53611; A53611.
DR   HSSP; P34996; 1DDD.
DR   GCRDb; GCR_0077; -.
DR   GCRDb; GCR_0610; -.
DR   GCRDb; GCR_1001; -.
DR   GCRDb; GCR_1339; -.
DR   GCRDb; GCR_1831; -.
DR   MIM; 146928; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN        1     48       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     49     75       1 (POTENTIAL).
FT   DOMAIN       76     84       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     85    105       2 (POTENTIAL).
FT   DOMAIN      106    120       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    121    142       3 (POTENTIAL).
FT   DOMAIN      143    163       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    164    183       4 (POTENTIAL).
FT   DOMAIN      184    208       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    209    231       5 (POTENTIAL).
FT   DOMAIN      232    251       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    252    273       6 (POTENTIAL).
FT   DOMAIN      274    294       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    295    315       7 (POTENTIAL).
FT   DOMAIN      316    360       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     22     22       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    119    196       BY SIMILARITY.
SQ   SEQUENCE   360 AA;  40759 MW;  564F04A8BCC0A197 CRC64;

  Query Match             29.4%;  Score 633;  DB 1;  Length 360;
  Best Local Similarity   40.1%;  Pred. No. 7.1e-37;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| ||||  |  |:|  |
Db      21 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
           | || :||:||:|| |  ||||:||      |:||: |||   |  :|||:| |||||
Db      80 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 139

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||         ||::||| || |||  :|    :
Db     140 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 189

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   :  :|      |  ||:|    ||:|||:|:|| :||   |  |  :   :
Db     190 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 245

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db     246 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 305

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           | |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db     306 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 357


RESULT 7
IL8B_MACMU
ID   IL8B_MACMU      STANDARD;      PRT;   353 AA.
AC   Q28519;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
GN   IL8RB OR CXCR2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96175151; PubMed=9110929;
RA   Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA   Lopez-Larrea C.;
RT   "Characterization of interleukin-8 receptors in non-human primates.";
RL   Immunogenetics 43:261-267(1996).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X91116; CAA62565.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   NON_TER       1      1
FT   DOMAIN       <1     45       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     46     72       1 (POTENTIAL).
FT   DOMAIN       73     81       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     82    102       2 (POTENTIAL).
FT   DOMAIN      103    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    139       3 (POTENTIAL).
FT   DOMAIN      140    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    180       4 (POTENTIAL).
FT   DOMAIN      181    205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    206    228       5 (POTENTIAL).
FT   DOMAIN      229    248       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    249    270       6 (POTENTIAL).
FT   DOMAIN      271    291       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    292    312       7 (POTENTIAL).
FT   DOMAIN      313   >353       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    116    193       BY SIMILARITY.
FT   CARBOHYD     19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     353    353
SQ   SEQUENCE   353 AA;  39947 MW;  EC8B38130657C713 CRC64;

  Query Match             29.3%;  Score 629.5;  DB 1;  Length 353;
  Best Local Similarity   40.3%;  Pred. No. 1.2e-36;
  Matches  143;  Conservative   51;  Mismatches  130;  Indels   31;  Gaps    7;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           |:| |:| |  :   |     ||  : ||  :: |:  :|:|:||| ||||  |  |:|
Db      15 EDF-SNYSYSSDLPPSLPDVAPCRPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILY 72
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Qy    128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
Db     73 SRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGIL 132

Qy    188 LLACISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLS 238
Db    133 LLACISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRR 182

Qy    239 AHHDERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVS 292
Db    183 TVYSSNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKA 238

Qy    293 RGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSG 352
Db    239 HMGQKHRAMRVIFAVVLIFLLCWLPYSLVLLADTLMRTQVIQETCERRNHIDRALDATEI 298

Qy    353 LGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSET 407
Db    299 LGILHSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHT 353
```

RESULT 8
IL8B_PANTR
ID IL8B_PANTR STANDARD; PRT; 353 AA.
AC Q28807;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
GN IL8RB OR CXCR2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96175151; PubMed=9110929;
RA Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA Lopez-Larrea C.;
RT "Characterization of interleukin-8 receptors in non-human primates.";
RL Immunogenetics 43:261-267(1996).
CC -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC --
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CC --
DR EMBL; X91113; CAA62563.1; -.
DR HSSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000832; GPCR_secretin.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Chemotaxis.
FT NON_TER 1 1
FT DOMAIN <1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 72 1 (POTENTIAL).
FT DOMAIN 73 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 117 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 180 4 (POTENTIAL).
FT DOMAIN 181 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 228 5 (POTENTIAL).
FT DOMAIN 229 248 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 249 270 6 (POTENTIAL).
FT DOMAIN 271 291 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 292 312 7 (POTENTIAL).
FT DOMAIN 313 >353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 116 193 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 353 353
SQ SEQUENCE 353 AA; 39998 MW; E745ACD9EC10C1E2 CRC64;

Query Match 28.9%; Score 622; DB 1; Length 353;
Best Local Similarity 39.6%; Pred. No. 4e-36;
Matches 139; Conservative 52; Mismatches 130; Indels 30; Gaps 6;

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Qy     72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
Db     18 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 76

Qy    132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
Db     77 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 136

Qy    192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
Db    137 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 186

Qy    243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
Db    187 SNVSPA-C---YEDMGNNTANWRMLLRMLPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 242

Qy    297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
Db    243 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHINRALDATEILGIL 302

Qy    357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSET 407
Db    303 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHT 353
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RESULT 9
IL8A_RABIT
ID IL8A_RABIT STANDARD; PRT; 355 AA.
AC P21109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE High affinity interleukin-8 receptor A (IL-8R A) (CXCR-1).
GN IL8RA OR CXCR1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91378994; PubMed=1898400;
RA Beckmann M.P., Munger W.E., Kozlosky C., Vandenbos T., Price V.,
RA Lyman S., Gerard N.P., Gerard C., Cerretti D.P.;
RT "Molecular characterization of the interleukin-8 receptor.";
RL Biochem. Biophys. Res. Commun. 179:784-789(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ALBINO; TISSUE=Neutrophils;
RX MEDLINE=91056034; PubMed=1700779;
RA Thomas K.M., Pyun H.Y., Navarro J.;
RT "Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.";
RL J. Biol. Chem. 265:20061-20064(1990).
RN [3]
RP SEQUENCE FROM N.A.

```
RC   TISSUE=Neutrophils;
RX   MEDLINE=92148149; PubMed=1737938;
RA   Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT   "Characterization of complementary DNA clones encoding the rabbit
RT   IL-8 receptor.";
RL   J. Immunol. 148:1261-1264(1992).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: NEUTROPHILS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -!- CAUTION: WAS ORIGINALLY (REF.2) THOUGHT TO BE THE RECEPTOR FOR
CC       FMET-LEU-PHE (N-FORMYL PEPTIDE RECEPTOR).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M74240; AAA31375.1; -.
DR   EMBL; M58021; AAA31377.1; -.
DR   EMBL; M82873; AAA31376.1; -.
DR   PIR; A23669; A23669.
DR   PIR; A46483; A46483.
DR   PIR; JQ1231; JQ1231.
DR   GCRDb; GCR_0107; -.
DR   GCRDb; GCR_0108; -.
DR   GCRDb; GCR_0298; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN       1     40       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    41     67       1 (POTENTIAL).
FT   DOMAIN      68     73       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    74     92       2 (POTENTIAL).
FT   DOMAIN      93    114       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   115    138       3 (POTENTIAL).
FT   DOMAIN     139    159       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   160    184       4 (POTENTIAL).
FT   DOMAIN     185    204       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   205    232       5 (POTENTIAL).
FT   DOMAIN     233    247       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   248    270       6 (POTENTIAL).
FT   DOMAIN     271    290       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   291    313       7 (POTENTIAL).
FT   DOMAIN     314    355       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     7      7       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    21     21       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   115    192       BY SIMILARITY.
FT   CONFLICT    90    111       DLLFALTMPIWAVSKEKGWIFG ->
FT                               PAFCPDHAYLGRLQGKRLDFR (IN REF. 2).
FT   CONFLICT   146    147       HA -> QS (IN REF. 2).
FT   CONFLICT   204    204       R -> C (IN REF. 2).
FT   CONFLICT   287    288       DI -> EL (IN REF. 2).
SQ   SEQUENCE   355 AA;  40622 MW;  EFE49ACB9D1E0F21 CRC64;

  Query Match             28.6%;  Score 615.5;  DB 1;  Length 355;
  Best Local Similarity   38.5%;  Pred. No. 1.1e-35;
  Matches  136;  Conservative   58;  Mismatches  130;  Indels   29;  Gaps    5;

Qy      69 NFSSSYDYGENESDSCCTSPPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVA 122
           |  :  : : |:|  :    ||  :|:|        ::  :  :|:|:||| ||||  |

Db       7 NMTDLWTWFEDEFANATGMPPVEKDYSPCLVVTQTLNKYVVVVIYALVFLLSLLGNSLVM 66

Qy     123 AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
            |:|  |:  | || :||:||:|| |  ||:|:|||     |:||: |||| : :||
Db      67 LVILYSRSNRSVTDVYLLNLAMADLLFALTMPIWAVSKEKGWIFGTPLCKVVSLVKEVNF 126

Qy     183 YAGALLLACISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPD 233
           |:| ||||||| |||| |||||:          |||         || :| | |: :||
Db     127 YSGILLLACISVDRYLAIVHATR----------TLTQKRHLVKFICLGIWALSLILSLPF 176

Qy     234 FIF---LSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           |:|    | ::   :      :|  :  |  ||:|    ||:|||||| :||   |  |
Db     177 FLFRQVFSPNNSSPVCYEDLGHNTAK-WRMVLRILPHTFGFILPLLVMLFCYGFTLRTLF 235

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
            :   :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |
Db     236 QAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTHVIQETCQRRNDIDRALDAT 295

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSS 403
             ||::| ||||::|||:|  ||     :|   |  ::  | |   :|   ||
Db     296 EILGFLHSCLNPIIYAFIGQNFRNGFLKMLAARGLISKEFLTRHRVTSYTSSS 348


RESULT 10
IL8B_RABIT
ID   IL8B_RABIT     STANDARD;      PRT;   358 AA.
AC   P35344;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
DE   receptor).
GN   IL8RB OR CXCR2.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ALBINO; TISSUE=Blood;
RX   MEDLINE=94230294; PubMed=8175642;
RA   Prado G.N., Thomas K.M., Suzuki H., Larosa G.J., Wilkinson N.C.,
RA   Folco E., Navarro J.;
RT   "Molecular characterization of a novel rabbit interleukin-8 receptor
RT   isotype.";
RL   J. Biol. Chem. 269:12391-12394(1994).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THE AFFINITY OF THIS RECEPTOR IS IL-8 >> NAP-2 >
CC       MGSA (GRO).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN NEUTROPHILS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L24445; AAA31378.1; -.
DR   PIR; A53752; A53752.
DR   GCRDb; GCR_0861; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
```

```
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN        1     46       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     47     73       1 (POTENTIAL).
FT   DOMAIN       74     82       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     83    103       2 (POTENTIAL).
FT   DOMAIN      104    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    140       3 (POTENTIAL).
FT   DOMAIN      141    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    181       4 (POTENTIAL).
FT   DOMAIN      182    206       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    207    229       5 (POTENTIAL).
FT   DOMAIN      230    249       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    250    271       6 (POTENTIAL).
FT   DOMAIN      272    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    313       7 (POTENTIAL).
FT   DOMAIN      314    358       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      8      8       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    117    194       BY SIMILARITY.
SQ   SEQUENCE   358 AA;  40632 MW;  6899716944D6126A CRC64;

  Query Match             28.6%;  Score 615;  DB 1;  Length 358;
  Best Local Similarity   39.7%;  Pred. No. 1.2e-35;
  Matches  141;  Conservative   55;  Mismatches  139;  Indels   20;  Gaps    6;

Qy      68 ENFS--------SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNG 119
           ||:|        |:| |  :   :   | ||  : ||  :   :   | |:||| ||||
Db       7 ENYSYEDFFGDFSNYSYSTDLPPTLLDSAPCRSE-SLETNSYVVLITYILVFLLSLLGNS 65

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  |:|  |:  | || :||:||:|| |   |||:||      | ||: ||||   :
Db      66 LVMLVILYSRSTCSVTDVYLLNLAIADLLFATTLPIWAASKVHGWTFGTPLCKVVSLVKE 125

Qy     180 INFYAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFL 237
           :|||:| ||||||| |||| |||||:  : :|     |   ||::||: |: :||  :|
Db     126 VNFYSGILLLACISVDRYLAIVHATRTMIQKR---HLVKFICLSMWGVSLILSLPILLFR 182

Qy     238 SAHHDERLNATHCQY----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSR 293
           :|      |::   |    |     |  ||:|    ||:|||||| :||   |  |  :
Db     183 NAIFPP--NSSPVCYEDMGNSTAKWRMVLRILPQTFGFILPLLVMLFCYVFTLRTLFQAH 240

Qy     294 GQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGL 353
           :: ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  |
Db     241 MGQKHRAMRVIFAVVLIFLLCWLPYNLVLLTDTLMRTHVIQETCERRNDIDRALDATEIL 300

Qy     354 GYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           |::| ||||::|||:| |||  :  :|   |  ::  | ::   |   ||   ||
Db     301 GFLHSCLNPIIYAFIGQKFRYGLLKILAAHGLISKEFLAKESRPSFVASSSGNTS 355


RESULT 11
IL8B_GORGO
ID   IL8B_GORGO     STANDARD;      PRT;   353 AA.
AC   Q28422;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (Fragment).
GN   IL8RB OR CXCR2.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96175151; PubMed=9110929;
RA   Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA   Lopez-Larrea C.;
RT   "Characterization of interleukin-8 receptors in non-human primates.";
RL   Immunogenetics 43:261-267(1996).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X91114; CAA62564.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   NON_TER       1      1
FT   DOMAIN       <1     45       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     46     72       1 (POTENTIAL).
FT   DOMAIN       73     81       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     82    102       2 (POTENTIAL).
FT   DOMAIN      103    117       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    118    139       3 (POTENTIAL).
FT   DOMAIN      140    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    161    180       4 (POTENTIAL).
FT   DOMAIN      181    205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    206    228       5 (POTENTIAL).
FT   DOMAIN      229    248       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    249    270       6 (POTENTIAL).
FT   DOMAIN      271    291       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    292    312       7 (POTENTIAL).
FT   DOMAIN      313   >353       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    116    193       BY SIMILARITY.
FT   CARBOHYD     19     19       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     353    353
SQ   SEQUENCE   353 AA;  39919 MW;  1FF04E31A7E825E4 CRC64;

  Query Match             28.5%;  Score 614;  DB 1;  Length 353;
  Best Local Similarity   39.3%;  Pred. No. 1.4e-35;
  Matches  138;  Conservative   52;  Mismatches  131;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| ||||  |  |:|  |
Db      18 SNYSYSSALPPFLLDASPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVILVILYSRVG 76

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
             | || :||:||:|| |  ||||:||      |:||: ||||   |  :|||:| |||||
Db      77 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 136

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:           |||          ||::||| || |||  :|    :
Db     137 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTIYP 186

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   :  :|       |  ||:|    ||::|||:| :||   |  |  :  :
Db     187 SNVSPV-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 242

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :: |   |  || :
Db     243 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHINQALDATEILGIL 302

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSET 407
           | ||||:|||:| ||   :  :|   |  ::  | :    |   ||   |
Db     303 HSCLNPLIYAFIGQKFCHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHT 353
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RESULT 12
IL8A_GORGO
ID   IL8A_GORGO     STANDARD;      PRT;   350 AA.
AC   P55919; P55921;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   High affinity interleukin-8 receptor A (IL-8R A) (IL-8 receptor type
DE   1) (CXCR-1) (CDW128).
GN   IL8RA OR CXCR1.
OS   Gorilla gorilla gorilla (Lowland gorilla), and
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595, 9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96175151; PubMed=9110929;
RA   Alvarez V., Coto E., Setien F., Gonzalez S., Gonzalez-Roces S.,
RA   Lopez-Larrea C.;
RT   "Characterization of interleukin-8 receptors in non-human primates.";
RL   Immunogenetics 43:261-267(1996).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO MGSA (GRO) WITH A LOW AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X91110; CAB37671.1; -.
DR   HSSP; P25024; 1ILP.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN        1     39       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     40     66       1 (POTENTIAL).
FT   DOMAIN       67     75       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     76     96       2 (POTENTIAL).
FT   DOMAIN       97    111       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    112    133       3 (POTENTIAL).
FT   DOMAIN      134    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    155    174       4 (POTENTIAL).
FT   DOMAIN      175    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    200    220       5 (POTENTIAL).
FT   DOMAIN      221    242       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    243    264       6 (POTENTIAL).
FT   DOMAIN      265    285       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    286    308       7 (POTENTIAL).
FT   DOMAIN      309    350       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     16     16       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    110    187       BY SIMILARITY.
SQ   SEQUENCE   350 AA;  39790 MW;  DB99591CD6C10757 CRC64;

  Query Match             28.5%;  Score 612.5;  DB 1;  Length 350;
  Best Local Similarity   40.0%;  Pred. No. 1.8e-35;
  Matches  136;  Conservative   50;  Mismatches  123;  Indels   31;  Gaps    5;

Qy      88 PPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH 141
           ||  :|:|         ::  :   |:| ||| |||| |  |:|  |   | || :||:
Db      21 PPIDEDYSPCRLETETLNKYVVIITYALAFLLSLLGNSLVMLVILYSRGGRSVTDVYLLN 80

Qy     142 LAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIV 201
           ||:|| |  ||||:||      |:||: ||||   |  :|||:| |||||| |||| ||
Db      81 LALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIV 140

Qy     202 HATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQY 252
           |||:          |||         ||  ||| :: :|| |:|  |:|   |::   |
Db     141 HATR----------TLTQKRHLVKFVCLGCWGLSMILSLPFFLFRQAYHPN--NSSPVCY 188

Qy     253 ----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
               |     |  ||:|    ||::|| || :||   |  |  :   :: ||||::  ||
Db     189 EVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVV 248

Qy     309 VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
           : | ||| ||:||:| | ||    :  :| | : | :|   |  ||::| ||||::|||:
Db     249 LIFLLCWLPYNLVLLADTLMRTQVIQESCERRNNVSLALDATEILGFLHSCLNPIIYAFI 308

Qy     369 GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           |  ||     :|   |  ::  | |   :|   || : :|
Db     309 GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348


RESULT 13
IL8B_BOVIN
ID   IL8B_BOVIN     STANDARD;      PRT;   360 AA.
AC   Q28003;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2).
GN   IL8RB OR CXCR2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li Y., Feng J., Templeton J.W.;
RL   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19947; AAA84996.1; -.
DR   GCRDb; GCR_1224; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN        1     48       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     49     75       1 (POTENTIAL).
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FT   DOMAIN       76     84       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     85    105       2 (POTENTIAL).
FT   DOMAIN      106    120       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    121    142       3 (POTENTIAL).
FT   DOMAIN      143    163       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    164    183       4 (POTENTIAL).
FT   DOMAIN      184    208       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    209    231       5 (POTENTIAL).
FT   DOMAIN      232    251       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    252    273       6 (POTENTIAL).
FT   DOMAIN      274    294       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    295    315       7 (POTENTIAL).
FT   DOMAIN      316    360       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    119    196       BY SIMILARITY.
FT   CARBOHYD     10     10       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     24     24       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   360 AA;  40625 MW;  9A7F70C982A632D1 CRC64;

  Query Match             28.2%;  Score 606;  DB 1;  Length 360;
  Best Local Similarity   38.4%;  Pred. No. 5.1e-35;
  Matches  141;  Conservative   54;  Mismatches  130;  Indels   42;  Gaps    6;

Qy      67 LENFSSSYDYGENESDSCCTSPPCPQDFSLN--------FDRAFLPALYSLLFLLGLLGN 118
           | | |  ::  |:|  :   :|| :|:  :         ::  :  : :|:||| ||||
Db       8 LSNSSILWEGFEDEFGNYSGTPP-TEDYDYSPCEISTETLNKYAVVVIDALVFLLSLLGN 66

Qy     119 GAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALF 178
             |  |:|  |   | || :||:||:|| |  :|||:|    |  ||||: ||||   |
Db      67 SLVMLVILYSRIGRSVTDVYLLNLAMADLLFAMTLPIWTASKAKGWVFGTPLCKVVSLLK 126

Qy     179 NINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLF 229
           :|||:| ||||||| |||| |||||:          |||          || :| | ::
Db     127 EVNFYSGILLLACISMDRYLAIVHATR----------TLTQKWHWVKFICLGIWALSVIL 176

Qy     230 ALPDFIFLSAHHD--------ERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYC 281
           ||| |||  |:          | | |   ::      |  :|||    |||||||||  :|
Db     177 ALPIFIFREAYQPPYSDLVCYEDLGANTTKW------RMIMRVLPQTFGFLLPLLVMLFC 230

Qy     282 YAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRES 341
           |   |  |  ::   : ||||::  ||: | ||| ||:||:: | ||    :|  | | :
Db     231 YGFTLRTLFSAQMGHKHRAMRVIFAVVLVFLLCWLPYNLVLIADTLMRAHVIAETCQRRN 290

Qy     342 RVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD 401
           :  |   |  ||:|| ||||||:| |:| |||  :  ::   |  ::  | :    |
Db     291 DIGRALDATEILGFLHSCLNPLIYVFIGQKFRHGLLKIMAIHGLISKEFLAKDGRPSFVG 350

Qy     402 SSWSETS 408
           ||   ||
Db     351 SSSGNTS 357


RESULT 14
IL8A_HUMAN
ID   IL8A_HUMAN     STANDARD;      PRT;   350 AA.
AC   P25024;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   High affinity interleukin-8 receptor A (IL-8R A) (IL-8 receptor type
DE   1) (CXCR-1) (CDw128a).
GN   IL8RA OR CXCR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91368199; PubMed=1840701;
RA   Holmes W.E., Lee J., Kuang W.-J., Rice G.C., Wood W.I.;
RT   "Structure and functional expression of a human interleukin-8
RT   receptor.";
RL   Science 253:1278-1280(1991).
RN   [2]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=93205012; PubMed=8384312;
RA   Cerretti D.P., Kozlosky C.J., Vanden Bos T., Nelson N., Gearing D.P.,
RA   Beckmann M.P.;
RT   "Molecular characterization of receptors for human interleukin-8,
RT   GRO/melanoma growth-stimulatory activity and neutrophil activating
RT   peptide-2.";
RL   Mol. Immunol. 30:359-367(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93252387; PubMed=8486366;
RA   Mollereau C., Passage E., Mattei M.-G., Vassart G., Parmentier M.;
RT   "The high-affinity interleukin 8 receptor gene (IL8RA) maps to the
RT   2q33-q36 region of the human genome: cloning of a pseudogene
RT   (IL8RBP) for the low-affinity receptor.";
RL   Genomics 16:248-251(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=95014476; PubMed=7929358;
RA   Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
RT   "Comparison of the genomic organization and promoter function for
RT   human interleukin-8 receptors A and B.";
RL   J. Biol. Chem. 269:26381-26389(1994).
RN   [5]
RP   CHARACTERIZATION.
RX   MEDLINE=92355587; PubMed=1379593;
RA   Lee J., Horuk R., Rice G.C., Bennett G.L., Camerato T., Wood W.I.;
RT   "Characterization of two high affinity human interleukin-8
RT   receptors.";
RL   J. Biol. Chem. 267:16283-16287(1992).
RN   [6]
RP   STRUCTURE BY NMR OF 9-29 IN COMPLEX WITH IL-8.
RX   MEDLINE=99148123; PubMed=10368283;
RA   Skelton N.J., Quan C., Reilly D., Lowman H.;
RT   "Structure of a CXC chemokine-receptor fragment in complex with
RT   interleukin-8.";
RL   Structure 7:157-168(1999).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO MGSA (GRO) WITH A LOW AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw128a entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw128a.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L19591; AAB59436.1; -.
DR   EMBL; L19592; AAA59160.1; -.
DR   EMBL; M68932; AAA59159.1; -.
DR   EMBL; X65858; CAA46688.1; -.
DR   EMBL; U11870; AAA64378.1; -.
DR   PIR; A39445; A39445.
DR   PDB; 1ILP; 23-DEC-98.
DR   PDB; 1ILQ; 23-DEC-98.
DR   GCRDb; GCR_0175; -.
DR   GCRDb; GCR_0696; -.
DR   GCRDb; GCR_1832; -.
DR   GCRDb; GCR_1833; -.
DR   GCRDb; GCR_2052; -.
DR   MIM; 146929; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
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DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis; Polymorphism; 3D-structure.
FT   DOMAIN        1     39       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     40     66       1 (POTENTIAL).
FT   DOMAIN       67     75       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     76     96       2 (POTENTIAL).
FT   DOMAIN       97    111       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    112    133       3 (POTENTIAL).
FT   DOMAIN      134    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    155    174       4 (POTENTIAL).
FT   DOMAIN      175    199       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    200    220       5 (POTENTIAL).
FT   DOMAIN      221    242       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    243    264       6 (POTENTIAL).
FT   DOMAIN      265    285       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    286    308       7 (POTENTIAL).
FT   DOMAIN      309    350       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      3      3       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     16     16       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    110    187       BY SIMILARITY.
FT   VARIANT     276    276       T -> S.
FT                                /FTId=VAR_003479.
SQ   SEQUENCE   350 AA;  39805 MW;  2463EEB51BEDD039 CRC64;

  Query Match             28.1%;  Score 605.5;  DB 1;  Length 350;
  Best Local Similarity   39.7%;  Pred. No. 5.4e-35;
  Matches  135;  Conservative   49;  Mismatches  125;  Indels   31;  Gaps    5;

Qy      88 PPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH 141
           ||  :|:|         ::  :   |:|:||| |||+  |  |:|  |   | || :||:
Db      21 PPADEDYSPCMLETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLN 80

Qy     142 LAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIV 201
           ||:|| |  ||||:||      |:||: ||||   |  :|||:| ||||||| |||| ||
Db      81 LALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIV 140

Qy     202 HATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQY 252
           |||:          |||           ||  ||| :  :|| |:|  |:|    |::   |
Db     141 HATR----------TLTQKRHLVKFVCLGCWGLSMNLSLPFFLFRQAYHPN--NSSPVCY 188

Qy     253 ----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
               |     |  ||:|    ||::|| || :||   |  |  :   :: ||||::  ||
Db     189 EVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVV 248

Qy     309 VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
           : | ||| ||:||:| | ||     :   | | : :  |   |  ||::| ||||::|||:
Db     249 LIFLLCWLPYNLVLLADTLMRTQVIQETCERRNNIGRALDATEILGFLHSCLNPIIYAFI 308

Qy     369 GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           |  ||     :|   |  ::  | |   :|   || : :|
Db     309 GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348


RESULT 15
IL8B_RAT
ID   IL8B_RAT       STANDARD;      PRT;   359 AA.
AC   P35407;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   High affinity interleukin-8 receptor B (IL-8R B) (CXCR-2) (GRO/MGSA
DE   receptor).
GN   IL8RB OR CXCR2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
RX   MEDLINE=97361587; PubMed=9218548;
RA   Gobl A.E., Huang M.R., Wang S., Zhou Y., Oeberg K.;
RT   "Molecular cloning and characterization of a cDNA encoding the rat
RT   interleukin-8 receptor.";
RL   Biochim. Biophys. Acta 1326:171-177(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Liver;
RA   Konishi K., Shibata F., Watanabe K., Tsurufuji S., Nakagawa H.,
RA   Fujioka M.;
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WISTAR; TISSUE=Spleen, and Lung;
RX   MEDLINE=97115810; PubMed=8955112;
RA   Dunstan C.-A.N., Salafranca M.N., Adhikari S., Xia Y., Feng L.,
RA   Harrison J.K.;
RT   "Identification of two rat genes orthologous to the human
RT   interleukin-8 receptors.";
RL   J. Biol. Chem. 271:32770-32776(1996).
CC   -!- FUNCTION: RECEPTOR TO INTERLEUKIN-8, WHICH IS A POWERFUL
CC       NEUTROPHILS CHEMOTACTIC FACTOR. BINDING OF IL-8 TO THE RECEPTOR
CC       CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED VIA A
CC       G-PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC       MESSENGER SYSTEM. THIS RECEPTOR BINDS TO IL-8 WITH A HIGH AFFINITY
CC       AND TO GRO/MGSA AND NAP-2 ALSO WITH A HIGH AFFINITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X77797; CAA54824.1; -.
DR   EMBL; D63584; BAA09797.1; -.
DR   EMBL; U70988; AAC52961.1; -.
DR   PIR; S42096; S42096.
DR   GCRDb; GCR_0913; -.
DR   GCRDb; GCR_1405; -.
DR   GCRDb; GCR_1524; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000832; GPCR_secretin.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein;
KW   Chemotaxis.
FT   DOMAIN        1     47       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     48     74       1 (POTENTIAL).
FT   DOMAIN       75     83       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     84    104       2 (POTENTIAL).
FT   DOMAIN      105    119       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    120    141       3 (POTENTIAL).
FT   DOMAIN      142    162       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    163    182       4 (POTENTIAL).
FT   DOMAIN      183    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    230       5 (POTENTIAL).
FT   DOMAIN      231    250       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    251    272       6 (POTENTIAL).
FT   DOMAIN      273    296       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    297    314       7 (POTENTIAL).
FT   DOMAIN      315    359       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      8      8       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     23     23       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    201    201       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    118    195       BY SIMILARITY.
SQ   SEQUENCE   359 AA;  40532 MW;  EF547326A074ABDD CRC64;
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Query Match 28.1%; Score 605; DB 1; Length 359;
Best Local Similarity 38.7%; Pred. No. 6e-35;
Matches 137; Conservative 58; Mismatches 139; Indels 20; Gaps 7;

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Qy      67 LENFSS----SYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVA 122
           ||:| |    ||:|  :   :   : |||   :|: :|  :  :| |: || |:||  |
Db      11 LEDFFSGDIDSYNYSSDPPFTLSDAAPCP-SANLDINRYAVVVIYVLVTLLSLVGNSLVM 69

Qy     123 AVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINF 182
            |:|  |:  | || :||:||:||    ||||:||      |:||| ||||   |  | |
Db      70 LVILYNRSTCSVTDVYLLNLAIADLFFALTLPVWAASKVNGWIFGSFLCKVFSFLQEITF 129

Qy     183 YAGALLLACISFDRYLNIVHATQ--LYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           |:  |||||| |||| |||||   : :|     |   |: :| | |: :|| || |
Db     130 YSSVLLLACISMDRYLAIVHATSTLIQKR---HLVKFVCITMWFLSLVLSLPIFI-LRTT 185

Qy     241 HDERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRG 294
           :   |  |   :|      |  ||:|    |||||||:| :||   |  |  :
Db     186 VKANPSTVVCYEN---IGNNTSKWRVVLRILPQTYGFLLPLLIMLFCYGFTLRTLFKAHM 242

Qy     295 QRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLG 354
            :: ||||::  ||: | ||| ||::|:  | ||    :   | |:: :: |   |  ||
Db     243 GQKHRAMRVIFAVVLVFLLCWLPYNIVLFTDTLMRTKLIKETCERQNEINKALEATEILG 302

Qy     355 YMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           ::| ||||::|||:| |||  :  ::   |  ::  | ::   |   || : ||
Db     303 FLHSCLNPIIYAFIGQKFRHGLLKIMANYGLVSKEFLAKEGRPSFVGSSSANTS 356
```

Search completed: November 2, 2002, 12:05:23
Job time : 28 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:04:45 ; Search time 71 Seconds
(without alignments)
1011.168 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1638.5	76.2	367	11	Q9JII9	Q9jii9 rattus norv
2	1629.5	75.8	367	11	Q9QWN6	Q9qwn6 mus musculu
3	603.5	28.1	392	13	O93281	O93281 gallus gall
4	585	27.2	358	13	Q9DGI1	Q9dgi1 gallus gall
5	577.5	26.8	347	6	Q9MZM7	Q9mzm7 callimico g
6	577	26.8	372	13	O93237	O93237 cyprinus ca
7	576.5	26.8	347	6	Q9MZN6	Q9mzn6 hylobates c
8	576.5	26.8	347	6	Q9MZN5	Q9mzn5 hylobates h
9	576.5	26.8	347	6	Q9MZN2	Q9mzn2 pongo pygma
10	576.5	26.8	347	6	Q9MZN1	Q9mzn1 gorilla gor
11	576.5	26.8	347	6	Q9MZM8	Q9mzm8 callithrix
12	576.5	26.8	347	6	Q9MZM1	Q9mzm1 eulemur mac
13	575.5	26.8	347	6	Q9MZP6	Q9mzp6 presbytis j
14	575.5	26.8	347	6	Q9MZP2	Q9mzp2 mandrillus
15	575.5	26.8	347	6	Q9MZM6	Q9mzm6 callicebus
16	574.5	26.7	334	6	Q9N1P3	Q9n1p3 hylobates l
17	574.5	26.7	347	6	Q9MZQ3	Q9mzq3 pygathrix a
18	574.5	26.7	347	6	Q9MZQ2	Q9mzq2 rhinopithec
19	574.5	26.7	347	6	Q9MZQ1	Q9mzq1 pygathrix b
20	574.5	26.7	347	6	Q9MZQ0	Q9mzq0 pygathrix n
21	574.5	26.7	347	6	Q9MZP9	Q9mzp9 nasalis lar
22	574.5	26.7	347	6	Q9MZP8	Q9mzp8 colobus pol
23	574.5	26.7	347	6	Q9MZP5	Q9mzp5 presbytis p
24	574.5	26.7	347	6	Q9MZP4	Q9mzp4 presbytis f
25	574.5	26.7	347	6	Q9MZP0	Q9mzp0 macaca assa
26	574.5	26.7	347	6	Q9MZN9	Q9mzn9 macaca arct
27	574.5	26.7	347	6	Q9MZN8	Q9mzn8 macaca thib
28	574.5	26.7	347	6	Q9MZN7	Q9mzn7 macaca neme
29	574.5	26.7	347	6	Q9MZN4	Q9mzn4 hylobates l
30	574.5	26.7	347	6	Q9MZN0	Q9mzn0 alouatta se
31	574.5	26.7	347	6	Q9MZM9	Q9mzm9 ateles pani
32	574	26.7	347	6	Q9MZP3	Q9mzp3 presbytis e
33	573.5	26.7	347	6	Q9MZN3	Q9mzn3 hylobates s
34	572.5	26.6	347	6	Q9MZP1	Q9mzp1 mandrillus
35	572.5	26.6	347	6	Q9MZM5	Q9mzm5 pithecia pi
36	572.5	26.6	352	4	Q9BXA0	Q9bxa0 homo sapien
37	572.5	26.6	352	6	Q9TSQ8	Q9tsq8 cercopithec
38	571.5	26.6	347	6	Q9MZP7	Q9mzp7 presbytis s
39	571	26.5	334	6	Q9N130	Q9n130 saimiri bol
40	571	26.5	346	6	Q9MZM4	Q9mzm4 nycticebus
41	571	26.5	346	6	Q9MZM3	Q9mzm3 nycticebus
42	571	26.5	346	6	Q9MZM2	Q9mzm2 nycticebus
43	570.5	26.5	352	6	O77488	O77488 cercopithec
44	567.5	26.4	352	6	Q9BDS5	Q9bds5 macaca fasc
45	566.5	26.3	334	6	Q9N1P4	Q9n1p4 cercopithec

ALIGNMENTS

RESULT 1
Q9JII9
ID Q9JII9 PRELIMINARY; PRT; 367 AA.
AC Q9JII9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CHEMOKINE RECEPTOR CXCR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20286573; PubMed=10825390;
RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S.,
RA Sarau H.M.;
RT "Identification and molecular characterization of rat CXCR3: receptor
RT expression and interferon-inducible protein-10 binding are increased
RT in focal stroke.";
RL Mol. Pharmacol. 57:1190-1198(2000).
DR EMBL; AF223642; AAF76982.1; -.
DR InterPro; IPR004070; CXCchemok_receptor3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01532; CXCCHMKINER3.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 367 AA; 40934 MW; F67C0362EDDBFCB7 CRC64;

Query Match 76.2%; Score 1638.5; DB 11; Length 367;
Best Local Similarity 86.3%; Pred. No. 1.4e-138;
Matches 315; Conservative 23; Mismatches 26; Indels 1; Gaps 1;

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Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||: |||: :::| |||| :| |||||||||    ||||||||||||| ||| |||||
Db       4 EVSERQVLDASDIAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPVLYSLL 62
```

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Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||:||||||||||||||||| |||||||||||||| ||||||||
Db     63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAAQWVFGSGL 122

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          |||||||||||||||| ||||||||||:||||||:||| |  || |||: |||||:|||
Db    123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPWVRVALTCIVVWGLCVLFA 182

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          |||||||| ||:||||||||||||||||||||||||||:|||||||||||||||||||
Db    183 LPDFIFLSASHDQRLNATHCQYNFPQVGRTALRVLQLVAGFLMPLLVMAYCYAHILAVLL 242

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||| ||||||||||||||:|||||||||||||||:| |||||||| ||||||||
Db    243 VSRGQRRFRAMRLVVVVVVAFAVCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVT 302

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||:|||||||||||||||||:|:|||||:|||  :||| |||||||||:||||||:||
Db    303 SGMGYMHCCLNPLLYAFVGVKFKEQMWMLLMRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy    411 SYSGL 415
          || ||
Db    363 SYLGL 367
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RESULT 2
Q9QWN6
ID Q9QWN6 PRELIMINARY; PRT; 367 AA.
AC Q9QWN6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE INTERFERON-INDUCIBLE PROTEIN 10 RECEPTOR.
GN CMKAR3 OR MCXCR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=99009219; PubMed=9790904;
RA Tamaru M., Tominaga Y., Yatunami K., Narumi S.;
RT "Cloning of the murine interferon-inducible protein 10 (IP-10)
RT receptor and its specific expression in lymphoid organs.";
RL Biochem. Biophys. Res. Commun. 251:41-48(1998).
DR EMBL; AB003174; BAA34045.1; -.
DR MGD; MGI:1277207; Cmkar3.
DR InterPro; IPR004070; CXCchemok_receptor3.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01532; CXCCHMKINER3.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;

Query Match 75.8%; Score 1629.5; DB 11; Length 367;
Best Local Similarity 86.3%; Pred. No. 8.9e-138;
Matches 315; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

```
Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||: |||: :: | |||| :| |||||||||    |||||||||||||| |||||||||
Db      4 EVSERQVLDASDFAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL 62

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||:||||||||||||||||| |||||||||||||||||||||| ||
Db     63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          |||||||||||||||| ||||||||||:||||||:||| |  || |||: |||||||||
Db    123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPWVRVALTCIVVWGLCVLFA 182

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          |||||||| ||:||||||||||||||||||||||||||:|||||||||||||||||||
Db    183 LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 242

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||| ||||||||||||||:|||||||||||||||:| |||||||| ||||||||
Db    243 VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRESHVDVAKSVT 302

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||:|||||||||||||||||:|:|||||:|||  :||| |||||||||:||||||:||
Db    303 SGMGYMHCCLNPLLYAFVGVKFREQMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy    411 SYSGL 415
          || ||
Db    363 SYLGL 367
```

RESULT 3
O93281
ID O93281 PRELIMINARY; PRT; 392 AA.
AC O93281;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE CHEMOKINE RECEPTOR.
GN CRL1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98244380; PubMed=9584981;
RA Gupta S.K., Pillarisetti K., Gray S.L., Stadel J.M.;
RT "Molecular cloning of a novel chemokine receptor-like gene from early
RT stage chick embryos.";
RL Biochem. Mol. Biol. Int. 44:673-681(1998).
DR EMBL; AF029369; AAC23950.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 2.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 392 AA; 44760 MW; 3B5CFCE88366F088 CRC64;

Query Match 28.1%; Score 603.5; DB 13; Length 392;
Best Local Similarity 36.9%; Pred. No. 7e-46;
Matches 133; Conservative 55; Mismatches 145; Indels 27; Gaps 5;

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Qy     72 SSYDYGENESDSCCTSPPCPQDFSLN-----------FDRAFLPALYSLLFLLGLLGNG 119
          | |   ||      |:|     |  |             | : |:|  | |:|:|| : |
Db     40 SGYYEAEN------TTPSLEGYFCFNPSSLWLANQRDPFRKVFIPLAYLLMFVLGTVQNA 93

Qy    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
            |  :|   : : ::|: || || :|:  |:|| |   |::   ||||: |||:  |:
Db     94 LVLVILERFKRSRTTTENFLFHLTLANLALLLTFPFSVVESLAGWVFGTFLCKILSAVHK 153

Qy    180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSA 239
          ||||           |||| ||:|   ||:     : ||| |:|   ||  ||| ||:
Db    154 INFYLHEHAAGLHRVDRYLAIVYAIHTYRKARARSIHLTCTAIWLSSLLLTLPDLIFMEV 213

Qy    240 HHDERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSR 293
            ||  | : |   ||: |        | | |    || :|||| ||| |:  |  |:
Db    214 WTDES-NRSICY--FPEAGIHGNNVWLATRFLYHSVGFFMPLLVMCYCYMAIVRTLCQSQ 270

Qy    294 GQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGL 353
            :| :|:|: ::|   | |||:|||:|: :: |  | | |::|  |  :| |  ||  :
Db    271 RLQRQKAVRVAILVTGVFLLCWSPYHIVIFLNTLTKLEAFAKDCLLEDHLDTAIMVTEAI 330

Qy    354 GYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYS 413
          |: ||||||::|||:|||||   : :|  ||| :|  ||     :|:       :  | |
```

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Db    331 GFTHCCLNPIIYAFIGVKFRNDFFRILHELGCISQETLQEILEVTRKGCGIESDNTTSIS 390


RESULT 4
Q9DGI1
ID   Q9DGI1      PRELIMINARY;      PRT;   358 AA.
AC   Q9DGI1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4.
GN   CXCR4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21089206; PubMed=11272281;
RA   Liang T.S., Hartt J.K., Lu S., Martins-Green M., Gao J.-L.,
RA   Murphy P.M.;
RT   "Cloning, mRNA distribution, and functional expression of an avian
RT   counterpart of the chemokine receptor/HIV coreceptor CXCR4.";
RL   J. Leukoc. Biol. 69:297-305(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF294794; AAG09054.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   358 AA;  40094 MW;  64E4977E29C86C9E CRC64;

  Query Match             27.2%;  Score 585;  DB 13;  Length 358;
  Best Local Similarity   35.8%;  Pred. No. 2.8e-44;
  Matches  123;  Conservative   65;  Mismatches  134;  Indels   22;  Gaps    5;

Qy      71 SSSY-DYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRR 129
           |: | ||||          || |  : :|:| ||| :||::|| |::||| |  |:  ::
Db      24 SADYGDYGE----------PCFQHENADFNRIFLPTIYSIIFLTGIIGNGLVIIVMGYQK 73

Qy     130 TALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLL 189
             | || : |||:||| | |:||| |:|||: | ||: |||    :: :| |:  |:|
Db      74 KQRSMTDKYRLHLSVADLLFVITLPFWSVDAAISWYFGNVLCKAVHVIYTVNLYSSVLIL 133

Qy     190 ACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATH 249
           | || |||| |||||   |        :  : ||   :|  :|| || |    |
Db     134 AFISLDRYLAIVHATNSQRPRKLLAEKIVYVGVWLPAVLLTVPDIIFASTSEVE--GRYL 191

Qy     250 CQYNFPQVG-RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
           |   :|      : |   :: | :|| |::  ||  |:: |  |:| :: :|::  |:::
Db     192 CDRMYPHDNWLISFRFQHILVGLVLPGLIILTCYCIIISKLSHSKGHQKRKALKTTVILI 251

Qy     309 VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
           : |  || ||:: : :|  : || :   |  :: |    |:|  | : ||||||:||||:
Db     252 LTFFACWLPYYIGISIDTFILLGVIRHRCSLDTIVHKWISITEALAFFHCCLNPILYAFL 311

Qy     369 GVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           | ||:      |        |::   ::||     |:    ||:
Db     312 GAKFKTSAQNALTSVSRGSSLKILSKSKRGGHSSVSTESESSSF 355


RESULT 5
Q9MZM7
ID   Q9MZM7      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZM7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Callimico goeldii (Goeldi's marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callimico.
OX   NCBI_TaxID=9495;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172236; AAF89356.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39269 MW;  A433F3D1BF7A4684 CRC64;

  Query Match             26.8%;  Score 577.5;  DB 6;  Length 347;
  Best Local Similarity   35.3%;  Pred. No. 1.3e-43;
  Matches  122;  Conservative   69;  Mismatches  140;  Indels   15;  Gaps    4;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| |||:||| |||||   | ||  |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLLVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| |||||   |       :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db     239 LILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           |:| ||:       |        |::   :||     |:    ||:
Db     299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 6
O93237
ID   O93237      PRELIMINARY;      PRT;   372 AA.
AC   O93237;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CXC CHEMOKINE RECEPTOR-1.
OS   Cyprinus carpio (Common carp).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC   Cypriniformes; Cyprinidae; Cyprinus.
OX   NCBI_TaxID=7962;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99367403; PubMed=10436187;
RA   Fujiki K., Shin D., Nakao M., Yano T.;
RT   "Molecular cloning of carp (Cyprinus carpio) CC chemokine, CXC
RT   chemokine receptors, allograft inflammatory factor-1, and natural
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RT   killer cell enhancing factor by use of suppression subtractive
RT   hybridization.";
RL   Immunogenetics 49:909-914(1999).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AB010468; BAA31458.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ   SEQUENCE   372 AA;  42258 MW;  B6ABD76BEFFE1B26 CRC64;

  Query Match             26.8%;  Score 577;  DB 13;  Length 372;
  Best Local Similarity   35.8%;  Pred. No. 1.6e-43;
  Matches  134;  Conservative   65;  Mismatches  149;  Indels   26;  Gaps    4;

Qy      57 VLNDAEVAALLENFSSSY----------DYGENESDSCCTSPPCPQDFSLNFDRAFLP 104
           :: |   :  ::|||  |           |:  :|    |:|    :  :: |
Db      10 MMTDPNSSLNIDNFSEFYDEFNYTDLLNMTDFVVDEKTLLCSSITMVKAVNIAF-----C 64

Qy     105 ALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQW 164
           | |:||: : ||  |  |: | : :||::| :| :| :|||| | ||  ||     |
Db      65 VFYVLIFLMAVPGNLIVGWVIASNKHSLSTSDVYLFNLMLADTLLALILPFSAVSVIHGW 124

Qy     165 VFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWG 224
           |||   ||:   :  :|||   | | ||| |||: || | :  :         :  |  ||
Db     125 VFGDIACKLVSLVKEVNFYTSILFLVCISVDRYMVIVRAMESRKARRRLCSGVACALVWF 184

Qy     225 LCLLFALPDF---IFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYC 281
           | |: :|| |    |  :   : : | | : |   : | | |: : : ||| ||:||  |
Db     185 LGLVLSLPSFYNEAFYESVSGQTVCAEHFETNHADIWRLATRITRHLLGFLFPLVVMLIC 244

Qy     282 YAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRES 341
           |:  :  || :|| :: |||:::: ||||| |||||:|:  : | |:    :  :|
Db     245 YSITVERLLRTRGFQKQRAMKVIIAVVVAFLLCWTPFHVSTIADTLLRAKVVRFSCFTRM 304

Qy     342 RVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRD 401
           ||||   |  || :|||:||:|||||| |||:|   :|      :::|:  : | ||
Db     305 VVDVAMYATQNLGLLHCCVNPVLYAFVGEKFRKRFLQML------HRKGVMERFSVSRSS 358

Qy     402 SSWSETSEASYSGL 415
           | | ||||  | |
Db     359 RSSSLTSEAPSSFL 372


RESULT 7
Q9MZN6
ID   Q9MZN6      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZN6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Hylobates concolor leucogyneus.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=101280;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172227; AAF89347.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39209 MW;  D853326462E15B22 CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.0%;  Pred. No. 1.6e-43;
  Matches  121;  Conservative   70;  Mismatches  140;  Indels   15;  Gaps    4;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : ||:: ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| ||||   |        :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |  :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|:: |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db     239 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           |:| ||:      |        |::    :||      |:    ||:
Db     299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 8
Q9MZN5
ID   Q9MZN5      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZN5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Hylobates hoolock (Hoolock gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=61851;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172228; AAF89348.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39209 MW;  D853326462E15B22 CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.0%;  Pred. No. 1.6e-43;
  Matches  121;  Conservative   70;  Mismatches  140;  Indels   15;  Gaps    4;
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Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : ||:: ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| |||||   |        :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db     239 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           |:| ||:      |        |::    :||     |:    ||:
Db     299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 9
Q9MZN2
ID   Q9MZN2      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZN2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172231; AAF89351.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39209 MW;  D853326462E15B22 CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.0%;  Pred. No. 1.6e-43;
  Matches  121;  Conservative   70;  Mismatches  140;  Indels   15;  Gaps    4;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : ||:: ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| |||||   |        :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db     239 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           |:| ||:      |        |::    :||     |:    ||:
Db     299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 10
Q9MZN1
ID   Q9MZN1      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZN1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Gorilla gorilla (gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9593;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172232; AAF89352.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39209 MW;  D853326462E15B22 CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.0%;  Pred. No. 1.6e-43;
  Matches  121;  Conservative   70;  Mismatches  140;  Indels   15;  Gaps    4;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : ||:: ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENANFNKIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| |||||   |        :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|||
Db     239 LILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
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          |:| ||:      |        |::    :||     |:    ||:
Db    299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 11
Q9MZM8
ID   Q9MZM8      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZM8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172235; AAF89355.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1       1
SQ   SEQUENCE   347 AA;  39152 MW;  925ECC9FC1E85753 CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.3%;  Pred. No. 1.6e-43;
  Matches  123;  Conservative   70;  Mismatches  136;  Indels   19;  Gaps    6;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEEIGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| ||||   | ||  |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVT--LTCLAVWGLCLLFALPDFIFLSAHHDERL 245
           :|| || |||| |||||   |  ||  :   :  : ||   ||  :|||||  |:  |
Db     121 ILASISLDRYLAIVHATTSQR--PPKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEAD 176

Qy     246 NATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLV 304
           :   |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::
Db     177 DRYICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTT 236

Qy     305 VVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLL 364
           |::::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:|
Db     237 VILILAFFACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPIL 296

Qy     365 YAFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           |||:| ||:      |        |::    :||     |:    ||:
Db     297 YAFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 12
Q9MZM1
ID   Q9MZM1      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZM1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Eulemur macaco (Petterus macaco).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Eulemur.
OX   NCBI_TaxID=30602;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172242; AAF89362.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1       1
SQ   SEQUENCE   347 AA;  39155 MW;  9BFA91A3824F7A7A CRC64;

  Query Match             26.8%;  Score 576.5;  DB 6;  Length 347;
  Best Local Similarity   35.2%;  Pred. No. 1.6e-43;
  Matches  122;  Conservative   68;  Mismatches  140;  Indels   17;  Gaps    5;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEELGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||  |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHH-DERLN 246
           :|| || |||| |||||   |    :   :    ||   ||  :|||||  |    |:|
Db     121 ILAFISLDRYLAIVHATNSQRPRKLSAEKVVYAGVWLPALLLTIPDFIFASVSEVDDRY- 179

Qy     247 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
              |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |
Db     180 --ICDRLYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 237

Qy     306 VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
           ::::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:||
Db     238 ILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILY 297

Qy     366 AFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           ||:| ||:      |        |::    :||     |:    ||:
Db     298 AFLGAKFKTSAQHALSSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 13
Q9MZP6
ID   Q9MZP6      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZP6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Presbytis johnii.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Presbytis.
OX   NCBI_TaxID=98375;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
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RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172217; AAF89337.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39145 MW;  D21B7BB4AF3DF693 CRC64;

  Query Match             26.8%;  Score 575.5;  DB 6;  Length 347;
  Best Local Similarity   34.9%;  Pred. No. 1.9e-43;
  Matches  121;  Conservative   71;  Mismatches  138;  Indels   17;  Gaps    5;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLS-AHHDERLN 246
           :|| || |||| |||||   :        :  : ||   ||  :|||| | :  |:|
Db     121 ILASISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEADDRY- 179

Qy     247 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |
Db     180 --ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 237

Qy     306 VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
           ::::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:||
Db     238 ILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILY 297

Qy     366 AFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
           ||:| ||:      |        |::    :||     |:    ||:
Db     298 AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 14
Q9MZP2
ID   Q9MZP2      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZP2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Mandrillus sphinx (Mandrill) (Papio sphinx).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Mandrillus.
OX   NCBI_TaxID=9561;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172221; AAF89341.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39189 MW;  0AE9600917D24874 CRC64;

  Query Match             26.8%;  Score 575.5;  DB 6;  Length 347;
  Best Local Similarity   34.9%;  Pred. No. 1.9e-43;
  Matches  121;  Conservative   71;  Mismatches  138;  Indels   17;  Gaps    5;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| |||||   | ||: |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGNFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLS-AHHDERLN 246
           :|| || |||| |||||   :        :  : ||   ||  :|||| | :  |:|
Db     121 ILAFISLDRYLAIVHATNSQKPRKLLAEKVVYVGVWIPALLLTIPDFIFASVSEADDRF- 179

Qy     247 ATHCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVV 305
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |
Db     180 --ICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLSHSKGHQKRKALKTTV 237

Qy     306 VVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLY 365
           ::::||  || ||:: : :|  : |  : : |  |: |    |:|  | : ||||||:||
Db     238 ILILAFFACWLPYYIGISIDSFILLEIIKQGCEFENTVHKWISITEALAFFHCCLNPILY 297

Qy     366 AFVGVKFRERMWMLL--------LRLGCPNQRGLQRQPSSSRRDSSW 404
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Db     298 AFLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSSF 344


RESULT 15
Q9MZM6
ID   Q9MZM6      PRELIMINARY;      PRT;   347 AA.
AC   Q9MZM6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR4 (FRAGMENT).
GN   CXCR4.
OS   Callicebus moloch (Dusky titi).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC   Callicebus.
OX   NCBI_TaxID=9523;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
RT   "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
RT   Primates.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF172237; AAF89357.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   347 AA;  39352 MW;  A4FECD8C61FC5AEA CRC64;

  Query Match             26.8%;  Score 575.5;  DB 6;  Length 347;
  Best Local Similarity   35.2%;  Pred. No. 1.9e-43;
  Matches  123;  Conservative   69;  Mismatches  138;  Indels   19;  Gaps    5;
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Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           :|::     |: :|       || :: : :|:| ||| :||::|| |::||| |  |:
Db       5 DNYTEEMGSGDYDS----IKEPCFREENAHFNRIFLPTIYSIIFLTGIVGNGLVILVMGY 60

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
           ::   | || : |||:||| | |:||| ||||    | ||  |||    :: :| |:  |
Db      61 QKKLRSMTDKYRLHLSVADLLFVITLPFWAVDAVANWYFGKFLCKAVHVIYTVNLYSSVL 120

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNA 247
           :|| || |||| |||||   |        :  : ||   ||  :|||||  |:  |  :
Db     121 ILAFISLDRYLAIVHATNSQRPRKLLAEKVVYVGVWIPALLLTIPDFIF--ANVSEADDR 178

Qy     248 THCQYNFP-QVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVV 306
             |   :|  :     :   :: | :|| :|:  ||  |:: |  |:| :: :|::  |:
Db     179 YICDRFYPNDLWVVVFQFQHIMVGLILPGIVILSCYCIIISKLTHSKGHQKRKALKTTVI 238

Qy     307 VVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYA 366
           :::||  || ||:: : :|  : |  : : |  |: |    |:|  | : |||||:|||
Db     239 LILAFIACWLPYYIGISIDSFILLEIIRQGCEFENTVHKWISITEALAFFHCCLNPILYA 298

Qy     367 FVGVKFRERMWMLL--------LRLGCPNQRG----LQRQPSSSRRDSS 403
           |:| ||:      |        |::    :||    :  :  |||  ||
Db     299 FLGAKFKTSAQHALTSVSRGSSLKILSKGKRGGHSSVSTESESSRFHSS 347
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Search completed: November 2, 2002, 12:06:56
Job time : 74 secs

GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:08:10 ; Search time 200 Seconds
(without alignments)
730.360 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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26: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2142	99.6	415	1	PCT-US96-00499-2	Sequence 2, Appli
2	2142	99.6	415	1	PCT-US96-00499A-2	Sequence 2, Appli
3	2142	99.6	415	15	US-09-101-518-2	Sequence 2, Appli
4	2136	99.3	472	1	PCT-US00-26524B-6392	Sequence 6392, Ap
5	1891	87.9	368	15	US-09-170-496-20	Sequence 20, Appl
6	1891	87.9	368	15	US-09-170-496C-20	Sequence 20, Appl
7	1891	87.9	368	15	US-09-170-496D-20	Sequence 20, Appl
8	1891	87.9	368	20	US-09-624-594-2	Sequence 2, Appli
9	1891	87.9	368	20	US-09-633-541-2	Sequence 2, Appli
10	1891	87.9	368	20	US-09-663-702-2	Sequence 2, Appli
11	1891	87.9	368	20	US-09-663-799-2	Sequence 2, Appli
12	1885	87.6	368	15	US-09-170-496C-174	Sequence 174, App
13	1885	87.6	368	15	US-09-170-496D-174	Sequence 174, App
14	1626.5	75.6	367	14	US-09-010-701C-22	Sequence 22, Appl
15	1519.5	70.6	380	26	US-60-258-273-107	Sequence 107, App
16	1281	59.6	271	26	US-60-213-169-424	Sequence 424, App
17	1281	59.6	271	26	US-60-213-170-424	Sequence 424, App
18	1197.5	55.7	970	26	US-60-212-655-534	Sequence 534, App
19	1172.5	54.5	944	26	US-60-229-515-947	Sequence 947, App
20	901	41.9	209	26	US-60-213-844-255	Sequence 255, App
21	661	30.7	357	1	PCT-US99-08395-20	Sequence 20, Appl
22	661	30.7	357	16	US-09-294-058-20	Sequence 20, Appl
23	637.5	29.6	399	1	PCT-US01-03800A-2394	Sequence 2394, Ap
24	637.5	29.6	399	1	PCT-US01-08631-43968	Sequence 43968, A
25	636.5	29.6	1490	26	US-60-207-317-223	Sequence 223, App
26	636	29.6	466	26	US-60-229-515-1218	Sequence 1218, Ap
27	636	29.6	466	26	US-60-229-515-1248	Sequence 1248, Ap
28	635.5	29.5	355	1	PCT-US01-16777-36	Sequence 36, Appl
29	635	29.5	372	12	US-08-802-627-6	Sequence 6, Appli
30	635	29.5	372	15	US-09-104-063-6	Sequence 6, Appli
31	635	29.5	372	15	US-09-170-496-66	Sequence 66, Appl
32	635	29.5	372	15	US-09-170-496C-66	Sequence 66, Appl
33	635	29.5	372	15	US-09-170-496D-66	Sequence 66, Appl
34	635	29.5	372	18	US-09-420-784-5	Sequence 5, Appli
35	635	29.5	372	19	US-09-573-353-5	Sequence 5, Appli
36	635	29.5	378	1	PCT-US01-03800A-2243	Sequence 2243, Ap
37	635	29.5	390	26	US-60-229-515-741	Sequence 741, App
38	634.5	29.5	355	1	PCT-US01-16777-37	Sequence 37, Appl
39	633	29.4	353	1	PCT-US96-00499-9	Sequence 9, Appli
40	633	29.4	353	1	PCT-US96-00499A-9	Sequence 9, Appli
41	633	29.4	353	15	US-09-101-518-9	Sequence 9, Appli
42	633	29.4	355	1	PCT-US01-16777-27	Sequence 27, Appl
43	633	29.4	355	1	PCT-US01-16777-28	Sequence 28, Appl
44	633	29.4	355	1	PCT-US01-16777-30	Sequence 30, Appl
45	633	29.4	355	1	PCT-US93-10672-4	Sequence 4, Appli

ALIGNMENTS

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RESULT 1
PCT-US96-00499-2
; Sequence 2, Application PC/TUS9600499
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;    TITLE OF INVENTION:  HSATU68
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00499
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-474
;    TELECOMMUNICATION INFORMATION:
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;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  415 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-00499-2

  Query Match             99.6%;  Score 2142;  DB 1;  Length 415;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-193;
  Matches  414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
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Db       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
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Db      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALNSLLFLLGLLGNGA 120

Qy     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240

Qy     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
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Db     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300

Qy     301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360

Qy     361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
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RESULT 2
PCT-US96-00499A-2
; Sequence 2, Application PC/TUS9600499A
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;    TITLE OF INVENTION:  HSATU68
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00499A
;      FILING DATE:  11 JAN 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-474
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  415 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US96-00499A-2

  Query Match             99.6%;  Score 2142;  DB 1;  Length 415;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-193;
  Matches  414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
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Db       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
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Qy     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
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Db     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180

Qy     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
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Qy     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
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Qy     361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
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RESULT 3
US-09-101-518-2
; Sequence 2, Application US/09101518
; GENERAL INFORMATION:
;  APPLICANT:  Li, Yi
;  TITLE OF INVENTION:  Human G-Protein Chemokine Receptor HSATU68
;  FILE REFERENCE:  PF218PCT.US
;  CURRENT APPLICATION NUMBER: US/09/101,518
;  CURRENT FILING DATE:  1998-12-21
;  PRIOR APPLICATION NUMBER:  PCT/US96/00499
;  PRIOR FILING DATE:  1996-01-11
;  NUMBER OF SEQ ID NOS:  9
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-101-518-2

  Query Match             99.6%;  Score 2142;  DB 15;  Length 415;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-193;
  Matches  414;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
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Db       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
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Db      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALNSLLFLLGLLGNGA 120
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Qy    121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
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Db    121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180

Qy    181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240

Qy    241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300

Qy    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360

Qy    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
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RESULT 4
PCT-US00-26524B-6392
; Sequence 6392, Application PC/TUS0026524B
; GENERAL INFORMATION:
; APPLICANT: Birse et. al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26524B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6392
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (139)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (164)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-26524B-6392

Query Match 99.3%; Score 2136; DB 1; Length 472;
Best Local Similarity 99.5%; Pred. No. 2.1e-192;
Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 117

Qy     61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
          |||||||||||||||||| |||||||||||||||||||| ||||||||||||
Db    118 AEVAALLENFSSSYDYGENESXSCCTSPPCPQDFSLNFDRAFLPALXSLLFLLGLLGNGA 177

Qy    121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 237

Qy    181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 297

Qy    241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 357

Qy    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 417

Qy    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 472
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RESULT 5
US-09-170-496-20
; Sequence 20, Application US/09170496
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496-20

Query Match 87.9%; Score 1891; DB 15; Length 368;
Best Local Similarity 99.7%; Pred. No. 2.1e-169;
Matches 364; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368
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RESULT 6
US-09-170-496C-20
; Sequence 20, Application US/09170496C
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040

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;  CURRENT APPLICATION NUMBER: US/09/170,496C
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496C-20

  Query Match            87.9%;  Score 1891;  DB 15;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 7
US-09-170-496D-20
; Sequence 20, Application US/09170496D
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-20

  Query Match            87.9%;  Score 1891;  DB 15;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 8
US-09-624-594-2
; Sequence 2, Application US/09624594
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/624,594
;      FILING DATE:  25-JUL-2000
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,838
;      FILING DATE:  10-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  368 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-624-594-2

  Query Match            87.9%;  Score 1891;  DB 20;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63
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Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 9
US-09-633-541-2
; Sequence 2, Application US/09633541
;  GENERAL INFORMATION:
;     APPLICANT:  Loetscher, Marcel
;     APPLICANT:  Moser, Bernhard
;     TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;     TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;       STREET:  Two Militia Drive
;       CITY:  Lexington
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02173
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/633,541
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/709,838
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brook Esq., David E.
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  TKI96-01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 861-6240
;       TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  368 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-633-541-2

  Query Match             87.9%;  Score 1891;  DB 20;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 10
US-09-663-702-2
; Sequence 2, Application US/09663702
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;                   Qin, Shixin
;                   Mackay, Charles R.
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,702
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/829,839
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 368 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-663-702-2
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  Query Match             87.9%;  Score 1891;  DB 20;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 11
US-09-663-799-2
; Sequence 2, Application US/09663799
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,799
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/709,838
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 368 amino acids
;             TYPE: amino acid
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-663-799-2

  Query Match             87.9%;  Score 1891;  DB 20;  Length 368;
  Best Local Similarity   99.7%;  Pred. No. 2.1e-169;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy     231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy     291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy     351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy     411 SYSGL 415
           |||||
Db     364 SYSGL 368


RESULT 12
US-09-170-496C-174
; Sequence 174, Application US/09170496C
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496C
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 174
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496C-174

  Query Match             87.6%;  Score 1885;  DB 15;  Length 368;
  Best Local Similarity   99.5%;  Pred. No. 7.7e-169;
  Matches  363;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
           :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy     111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy     171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183
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Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAKRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 13
US-09-170-496D-174
; Sequence 174, Application US/09170496D
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 174
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-174

  Query Match             87.6%;  Score 1885;  DB 15;  Length 368;
  Best Local Similarity   99.5%;  Pred. No. 7.7e-169;
  Matches  363;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAKRLVVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 14
US-09-010-701C-22
; Sequence 22, Application US/09010701C
;  GENERAL INFORMATION:
;    APPLICANT:  Mattson, Jeanine D.
;    APPLICANT:  Soto-Trejo, Hortensia
;    APPLICANT:  Hedrick, Joseph A.
;    APPLICANT:  Gorman, Daniel M.
;    APPLICANT:  Zlotnik, Albert
;    TITLE OF INVENTION:  Mammalian Chemokines; Receptors;
;    TITLE OF INVENTION:  Reagents; Uses
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/010,701C
;      FILING DATE:  22-JAN-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/036,715
;      FILING DATE:  23-JAN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0689
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1200
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  367 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-010-701C-22

  Query Match             75.6%;  Score 1626.5;  DB 14;  Length 367;
  Best Local Similarity   86.0%;  Pred. No. 2e-144;
  Matches  314;  Conservative   22;  Mismatches   28;  Indels    1;  Gaps    1;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||: |||: :: | |||| :| |||||||||    |||||||||||||| |||||||||
Db      4 EVSERQVLDASDFAFLLENSTSPYDYGENESD-FSDSPPCPQDFSLNFDRTFLPALYSLL 62

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||:|||||||||||||||| |||||||||||||||||| ||
Db     63 FLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLVLTLPLWAVDAAVQWVFGPGL 122

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          |||||||||||||||| ||||||||||:||||||||| |  || ||||: |||||||||
Db    123 CKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYRRDPRVRVALTCIVVWGLCLLFA 182

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          |||||:|||::|:|||||||||||||||||||||||||||||||||||||||||||||||
Db    183 LPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 242

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||| |||||||||| |||:||||||||||||||:| |||||||:| ||||||||
Db    243 VSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLVDILMDVGVLARNCGRKSHVDVAKSVT 302

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||:|||||||||||||||||:|||| |||  :||| |||||||||:||||||:||
Db    303 SGMGYMHCCLNPLLYAFVGVKFREKMWMLFTRLGRSDQRGPQRQPSSSRRESSWSETTEA 362

Qy    411 SYSGL 415
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          || ||
Db    363 SYLGL 367


RESULT 15
US-60-258-273-107
; Sequence 107, Application US/60258273
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
;  TITLE OF INVENTION:  HORMONE RECEPTOR PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001042-PROV
;  CURRENT APPLICATION NUMBER: US/60/258,273
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 107
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Human
US-60-258-273-107

  Query Match             70.6%;  Score 1519.5;  DB 26;  Length 380;
  Best Local Similarity   92.1%;  Pred. No. 2.6e-134;
  Matches  302;  Conservative    5;  Mismatches   12;  Indels    9;  Gaps    2;

Qy     41 TAPS----SPFPPSQVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSL 96
          | ||    ||    :|||||||||||||||||||||||||||||||||||||||||||||
Db     12 TPPSSQSTSPAMVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSL 71

Qy     97 NFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLW 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 NFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLW 131

Qy    157 AVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVT 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 AVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVT 191

Qy    217 LTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLL 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 LTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLL 251

Qy    277 VMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARN 336
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Db    252 VMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARN 311

Qy    337 CGRESRVDVAKSVTSGLGYMHCCLNPLL 364
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Db    312 CGRESRV-----VRGQVGHLRPGLHALL 334


Search completed: November  2, 2002, 12:14:54
Job time : 203 secs
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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: November 2, 2002, 12:07:05 ; Search time 123 Seconds
(without alignments)
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Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1112697 seqs, 300604653 residues

Total number of hits satisfying chosen parameters: 1112697

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep1:*
3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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10: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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12: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
13: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2151	100.0	415	9	US-09-101-518A-2	Sequence 2, Appli
2	2136	99.3	472	11	US-10-106-698-6402	Sequence 6402, Ap
3	1891	87.9	368	11	US-10-251-686-2	Sequence 2, Appli
4	1891	87.9	368	11	US-10-251-385-20	Sequence 20, Appl
5	1885	87.6	368	11	US-10-251-385-174	Sequence 174, App
6	661	30.7	357	9	US-09-694-401A-20	Sequence 20, Appl
7	661	30.7	357	11	US-10-224-855-20	Sequence 20, Appl
8	635	29.5	372	11	US-10-251-385-66	Sequence 66, Appl
9	633	29.4	353	9	US-09-101-518A-9	Sequence 9, Appli
10	633	29.4	355	9	US-09-625-573-8	Sequence 8, Appli
11	633	29.4	360	2	PCT-US02-07946A-16	Sequence 16, Appl
12	633	29.4	360	11	US-10-099-007A-16	Sequence 16, Appl
13	633	29.4	372	11	US-10-251-385-200	Sequence 200, App
14	610	28.4	377	11	US-10-143-982-194	Sequence 194, App
15	606.5	28.2	350	2	PCT-US02-15638-3	Sequence 3, Appli
16	606.5	28.2	350	2	PCT-US02-07946A-15	Sequence 15, Appl
17	606.5	28.2	350	11	US-10-099-007A-15	Sequence 15, Appl
18	605.5	28.1	350	9	US-09-625-573-7	Sequence 7, Appli
19	602	28.0	378	11	US-10-143-982-290	Sequence 290, App
20	602	28.0	378	11	US-10-211-364-780	Sequence 780, App
21	602	28.0	378	11	US-10-212-054-862	Sequence 862, App
22	602	28.0	378	11	US-10-213-073-338	Sequence 338, App
23	602	28.0	378	11	US-10-216-428-142	Sequence 142, App
24	602	28.0	378	11	US-10-216-436-526	Sequence 526, App
25	602	28.0	378	11	US-10-216-893-220	Sequence 220, App
26	602	28.0	378	11	US-10-219-917-240	Sequence 240, App
27	588	27.3	399	11	US-10-143-982-244	Sequence 244, App
28	586	27.2	378	9	US-09-694-401A-13	Sequence 13, Appl
29	586	27.2	378	11	US-10-224-855-13	Sequence 13, Appl
30	586	27.2	378	11	US-10-251-385-74	Sequence 74, Appl
31	584	27.2	359	9	US-09-646-785A-3	Sequence 3, Appli
32	584	27.2	378	11	US-10-251-385-204	Sequence 204, App
33	577.5	26.8	352	9	US-09-625-573-6	Sequence 6, Appli
34	576.5	26.8	352	2	PCT-US01-51165-126	Sequence 126, App
35	576.5	26.8	352	9	US-09-813-651B-85	Sequence 85, Appl
36	576.5	26.8	352	9	US-09-646-785A-1	Sequence 1, Appli
37	576.5	26.8	352	9	US-09-647-501-2	Sequence 2, Appli
38	576.5	26.8	352	11	US-10-151-274-4	Sequence 4, Appli
39	576.5	26.8	352	11	US-10-160-401-3	Sequence 3, Appli
40	576.5	26.8	352	11	US-10-014-322A-126	Sequence 126, App
41	570.5	26.5	353	11	US-10-143-982-200	Sequence 200, App
42	567.5	26.4	378	9	US-09-694-401A-16	Sequence 16, Appl
43	567.5	26.4	378	11	US-10-224-855-16	Sequence 16, Appl
44	566.5	26.3	378	11	US-10-164-649-5	Sequence 5, Appli
45	566	26.3	378	9	US-09-686-020A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-101-518A-2
; Sequence 2, Application US/09101518A
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
; FILE REFERENCE: PF218US
; CURRENT APPLICATION NUMBER: US/09/101,518A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: PCT/US96/00499
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-101-518A-2

Query Match 100.0%; Score 2151; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 6.1e-174;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60

Qy      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120

Qy     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180

Qy     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240

Qy     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
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Qy    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360

Qy    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415


RESULT 2
US-10-106-698-6402
; Sequence 6402, Application US/10106698
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6402
;   LENGTH: 472
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (139)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (164)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-6402

  Query Match            99.3%;  Score 2136;  DB 11;  Length 472;
  Best Local Similarity  99.5%;  Pred. No. 1.3e-172;
  Matches  413;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     58 MELRKYGPGRLAGTVIGGAAQSKSQTKSDSITKEFLPGLYTAPSSPFPPSQVSDHQVLND 117

Qy     61 AEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGA 120
          ||||||||||||||||||| |||||||||||||||||||||| ||||||||||||
Db    118 AEVAALLENFSSSYDYGENESXSCCTSPPCPQDFSLNFDRAFLPALXSLLFLLGLLGNGA 177

Qy    121 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 VAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNI 237

Qy    181 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 NFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFLSAH 297

Qy    241 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 HDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRA 357

Qy    301 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 MRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCL 417

Qy    361 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 415
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 NPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEASYSGL 472


RESULT 3
```

```
US-10-251-686-2
; Sequence 2, Application US/10251686
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;                   Qin, Shixin
;                   Mackay, Charles R.
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/251,686
;             FILING DATE: 20-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/829,839
;             FILING DATE: 31-MAR-1997
;             APPLICATION NUMBER: US 08/709,838
;             FILING DATE: 10-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 368 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-251-686-2

  Query Match            87.9%;  Score 1891;  DB 11;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 5.8e-152;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 4
US-10-251-385-20
; Sequence 20, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-251-385-20

  Query Match            87.9%;  Score 1891;  DB 11;  Length 368;
  Best Local Similarity  99.7%;  Pred. No. 5.8e-152;
  Matches  364;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 5
US-10-251-385-174
; Sequence 174, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 174
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-251-385-174

  Query Match            87.6%;  Score 1885;  DB 11;  Length 368;
  Best Local Similarity  99.5%;  Pred. No. 1.9e-151;
  Matches  363;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     51 QVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 110
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 EVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLL 63

Qy    111 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 FLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGL 123

Qy    171 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 CKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFA 183

Qy    231 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 LPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLL 243

Qy    291 VSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 350
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 VSRGQRRLRAKRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVT 303

Qy    351 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 SGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEA 363

Qy    411 SYSGL 415
          |||||
Db    364 SYSGL 368


RESULT 6
US-09-694-401A-20
; Sequence 20, Application US/09694401A
; GENERAL INFORMATION:.
;  APPLICANT: Gonzalo, Jose Angel
;  APPLICANT:  Gutierrez-Ramos, Jose Carlos
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE BGCKR-RELATED PROTEIN FAMILY AND USES T
;  FILE REFERENCE: 07334-317001
;  CURRENT APPLICATION NUMBER: US/09/694,401A
;  CURRENT FILING DATE:  2000-10-23
;  PRIOR APPLICATION NUMBER: US 09/294,058
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: US 09/061,753
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 357
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus sequence
US-09-694-401A-20

  Query Match            30.7%;  Score 661;  DB 9;  Length 357;
  Best Local Similarity  40.1%;  Pred. No. 1e-47;
  Matches  141;  Conservative   65;  Mismatches  122;  Indels   24;  Gaps    6;
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Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           || :|  || : |         | ::   || : ||| :|||:|::|||||  |
Db      12 ENTTSYVDYSQYEL-------LCSKEDVRNFAKVFLPIMYSLIFVVGLLGNSLVVLTYAY 64

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
             :   : || :||:||||| | :|||| ||| ||  ||||  :||:   :: :|| :| |
Db      65 YKKLRTMTDVYLLNLAVADLLFLLTLPFWAVSAAHGWVFGVAMCKLLSGIYTVNFVSGML 124

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTL----TCLAVWGLCLLFALPDFIFLSAHHDE 243
           |||||| |||: || ||  :|    :|| |     |: || | :| ::|: :| :   :|
Db     125 LLACISIDRYIAIVQATSAHRH--RSRVLLISKVICVGVWVLAILLSIPELVFSTV--NE 180

Qy     244 RLNATHCQYNFPQVGRTALRV----LQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLR 299
                 |   :|    |||:     |::| || :||| ||:||  |:  || ::  :| :
Db     181 LSGDVRCSPIYPSSEGTALKALIQGLEMVIGFFVPLLAMAFCYLIIIKTLLQAQNSKRHK 240

Qy     300 AMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCC 359
           |:::: ||| | :  ||: |:||  : ::| |  :|    ::|:|  ||  | ::|||
Db     241 ALKVIIAVVVVFIVTQLPYNGVLLVQTIANIGILISSCETSKQLDIAIQVTESLAFLHCC 300

Qy     360 LNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |||:||||:|||||  :  |   |||     |:|:  || |    | : | |
Db     301 LNPVLYAFIGVKFRNYLMKLAKDLGC-----LRREQWSSARHRESSISREFS 347


RESULT 7
US-10-224-855-20
; Sequence 20, Application US/10224855
; GENERAL INFORMATION:
;  APPLICANT: Gonzalo, Jose Angel
;  APPLICANT:  Gutierrez-Ramos, Jose Carlos
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE BGCKR-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 07334-317001
;  CURRENT APPLICATION NUMBER: US/10/224,855
;  CURRENT FILING DATE:  2002-08-21
;  PRIOR APPLICATION NUMBER: US/09/694,401
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 09/294,058
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: US 09/061,753
;  PRIOR FILING DATE: 1998-04-16
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 357
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus sequence
US-10-224-855-20

  Query Match             30.7%;  Score 661;  DB 11;  Length 357;
  Best Local Similarity   40.1%;  Pred. No. 1e-47;
  Matches  141;  Conservative   65;  Mismatches  122;  Indels   24;  Gaps    6;

Qy      68 ENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLS 127
           || :|  || : |         | ::   || : ||| :|||:|::|||||  |
Db      12 ENTTSYVDYSQYEL-------LCSKEDVRNFAKVFLPIMYSLIFVVGLLGNSLVVLTYAY 64

Qy     128 RRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGAL 187
             :   : || :||:||||| | :|||| ||| ||  ||||  :||:   :: :|| :| |
Db      65 YKKLRTMTDVYLLNLAVADLLFLLTLPFWAVSAAHGWVFGVAMCKLLSGIYTVNFVSGML 124

Qy     188 LLACISFDRYLNIVHATQLYRRGPPARVTL----TCLAVWGLCLLFALPDFIFLSAHHDE 243
           |||||| |||: || ||  :|    :|| |     |: || | :| ::|: :| :   :|
Db     125 LLACISIDRYIAIVQATSAHRH--RSRVLLISKVICVGVWVLAILLSIPELVFSTV--NE 180

Qy     244 RLNATHCQYNFPQVGRTALRV----LQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLR 299
                 |   :|    |||:     |::| || :||| ||:||  |:  || ::  :| :
Db     181 LSGDVRCSPIYPSSEGTALKALIQGLEMVIGFFVPLLAMAFCYLIIIKTLLQAQNSKRHK 240

Qy     300 AMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCC 359
           |:::: ||| | :  ||: |:||  : ::| |  :|    ::|:|  ||  | ::|||
Db     241 ALKVIIAVVVVFIVTQLPYNGVLLVQTIANIGILISSCETSKQLDIAIQVTESLAFLHCC 300

Qy     360 LNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           |||:||||:|||||  :  |   |||     |:|:  || |    | : | |
Db     301 LNPVLYAFIGVKFRNYLMKLAKDLGC-----LRREQWSSARHRESSISREFS 347


RESULT 8
US-10-251-385-66
; Sequence 66, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-251-385-66

  Query Match             29.5%;  Score 635;  DB 11;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 1.7e-45;
  Matches  147;  Conservative   50;  Mismatches  145;  Indels   18;  Gaps    8;

Qy      67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
           |||    :   |  :| :| |   :  ||        :|   |:|  |||:||||::||
Db      11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy     120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
           |  :|   |  |||:||| |||||| |||  ||    : :| || |: |||   ||
Db      71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy     180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
           :|||  :||||||: |||| ||||   ||       : :||  :| :  | |||: :|
Db     131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy     238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
            ||:  |    | ::       |       | |  |||||||:||| :||  ::  |
Db     191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy     292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
           |  :| :|:|: ::|    | |||:|||:|: :| |  | |:   |      : || ::
Db     249 QRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy     352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
           ||  ||||||:|| | ||||  :  || :|||     | :   | || || ||:  |:
Db     309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 9
US-09-101-518A-9
; Sequence 9, Application US/09101518A
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
;  FILE REFERENCE: PF218US
;  CURRENT APPLICATION NUMBER: US/09/101,518A
;  CURRENT FILING DATE:  2002-03-18
;  PRIOR APPLICATION NUMBER: PCT/US96/00499
;  PRIOR FILING DATE: 1996-01-11
;  NUMBER OF SEQ ID NOS: 9
```

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-101-518A-9

  Query Match             29.4%;  Score 633;  DB 9;  Length 353;
  Best Local Similarity   40.1%;  Pred. No. 2.4e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| |||| | |:|  |
Db      15 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 73

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
            | || :||:||:|| |  ||||:||      |:||: |||| | :|||:| |||||
Db      74 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 133

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||          ||::||| || |||  :|    :
Db     134 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 183

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   : :|       |  ||:|    ||::|||:| :||   |  |  :   :
Db     184 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 239

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db     240 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 299

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           | |||||:|||:| |||  :  :|   |  ::  | :    |   ||   ||
Db     300 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 351


RESULT 10
US-09-625-573-8
; Sequence 8, Application US/09625573
;   GENERAL INFORMATION:
;        APPLICANT: Charo, Israel
;                   Coughlin, Shaun
;        TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
;                            PROTEIN RECEPTORS
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
;             STREET: 5 Palo Alto Square
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94306-2155
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/625,573
;             FILING DATE: 25-Jul-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/446,669
;             FILING DATE: May 25, 1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Neeley, Richard
;             REGISTRATION NUMBER: 30,092
;             REFERENCE/DOCKET NUMBER: UCAL-237/01US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-843-5000
;             TELEFAX: 415-857-0663
;             TELEX: 380816CooleyPA
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 355 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: NO
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-625-573-8

  Query Match             29.4%;  Score 633;  DB 9;  Length 355;
  Best Local Similarity   40.1%;  Pred. No. 2.4e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| |||| | |:|  |
Db      16 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 74

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
            | || :||:||:|| |  ||||:||      |:||: |||| | :|||:| |||||
Db      75 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 134

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||          ||::||| || |||  :|    :
Db     135 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 184

Qy     243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
             ::   |   : :|       |  ||:|    ||::|||:| :||   |  |. :   :
Db     185 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 240

Qy     297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
           : ||||::  ||: | ||| ||:||:| | ||    :   | | : :| |   |  || :
Db     241 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 300

Qy     357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
           | |||||:|||:| |||  :  :|   |  :: ' | :    |   ||   ||
Db     301 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 352


RESULT 11
PCT-US02-07946A-16
; Sequence 16, Application PC/TUS0207946A
; GENERAL INFORMATION:
;  APPLICANT: Theodore Torphy
;  TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULMONARY DISEASE-RELATED
;  TITLE OF INVENTION:  IMMUNOGLOBULIN
;  TITLE OF INVENTION:  DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN-0286 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/07946A
;  CURRENT FILING DATE:  2002-03-14
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 16
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-07946A-16

  Query Match             29.4%;  Score 633;  DB 2;  Length 360;
  Best Local Similarity   40.1%;  Pred. No. 2.4e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy      72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
           |:| |          : ||  : ||  :: |:  :|:|:||| |||| | |:|  |
Db      21 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79

Qy     132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
            | || :||:||:|| |  ||||:||      |:||: |||| | :|||:| |||||
Db      80 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 139

Qy     192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
           || |||| |||||:          |||          ||::||| || |||  :|    :
Db     140 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 189
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Qy    243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
Db    190 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 245

Qy    297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
Db    246 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 305

Qy    357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
Db    306 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 357


RESULT 12
US-10-099-007A-16
; Sequence 16, Application US/10099007A
; GENERAL INFORMATION:
;  APPLICANT: Theodore Torphy
;  TITLE OF INVENTION: CHRONIC OBSTRUCTIVE PULOMARY DISEASE-RELATED IMMUNOGLOBULIN
;  TITLE OF INVENTION:  DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
;  FILE REFERENCE: CEN-0286
;  CURRENT APPLICATION NUMBER: US/10/099,007A
;  CURRENT FILING DATE:  2002-03-14
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 16
;   LENGTH: 360
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-099-007A-16

  Query Match             29.4%;  Score 633;  DB 11;  Length 360;
  Best Local Similarity   40.1%;  Pred. No. 2.4e-45;
  Matches  141;  Conservative   51;  Mismatches  130;  Indels   30;  Gaps    6;

Qy     72 SSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTA 131
Db     21 SNYSYSSTLPPFLLDAAPCEPE-SLEINKYFVVIIYALVFLLSLLGNSLVMLVILYSRVG 79

Qy    132 LSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLAC 191
Db     80 RSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLAC 139

Qy    192 ISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHD 242
Db    140 ISVDRYLAIVHATR----------TLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYS 189

Qy    243 ERLNATHCQYNFPQVG------RTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQR 296
Db    190 SNVSPA-C---YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQ 245

Qy    297 RLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYM 356
Db    246 KHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEILGIL 305

Qy    357 HCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
Db    306 HSCLNPLIYAFIGQKFRHGLLKILAIHGLISKDSLPKDSRPSFVGSSSGHTS 357


RESULT 13
US-10-251-385-200
; Sequence 200, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-251-385-200

  Query Match             29.4%;  Score 633;  DB 11;  Length 372;
  Best Local Similarity   40.8%;  Pred. No. 2.5e-45;
  Matches  147;  Conservative   49;  Mismatches  146;  Indels   18;  Gaps    8;

Qy     67 LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLLGLLGNG 119
Db     11 LENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSLIFLLGVIGNV 70

Qy    120 AVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFN 179
Db     71 LVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTFLCKTVIALHK 130

Qy    180 INFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLFALPDFIFL-- 237
Db    131 VNFYCSSLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFLLALPEILFAKV 190

Qy    238 -SAHHDERLNATHCQYNFPQVGRT----ALRVLQLVAGFLLPLLVMAYCYAHILAVL-LV 291
Db    191 SQGHHNNSL--PRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVGVVHRLRQA 248

Qy    292 SRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTS 351
Db    249 QRRPQRQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSLPVAITMCE 308

Qy    352 GLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETSEAS 411
Db    309 FLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRR-SSLSESENAT 367


RESULT 14
US-10-143-982-194
; Sequence 194, Application US/10143982
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ38C1N
;  CURRENT APPLICATION NUMBER: US/10/143,982
;  CURRENT FILING DATE:  2002-05-14
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 396
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
;   LENGTH: 377
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-143-982-194

  Query Match             28.4%;  Score 610;  DB 11;  Length 377;
  Best Local Similarity   38.9%;  Pred. No. 2.3e-43;
  Matches  142;  Conservative   48;  Mismatches  129;  Indels   46;  Gaps    7;

Qy     78 ENESDSCCTSPPCPQDF-SLNF------DRAFLPAL--------------YSLLFLLGLL 116
Db     23 ETEEDMSNITDPQMWDFDDLNFTGMPPADEDYSPCMLETETLNKYVVIIAYALVFLLSLL 82

Qy    117 GNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGA 176
Db     83 GNSLVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPIWAASKVNGWIFGTFLCKVVSL 142

Qy    177 LFNINFYAGALLLACISFDRYLNIVHATQLYRRGPPARVTLT---------CLAVWGLCL 227
Db    143 LKEVNFYSGILLLACISVDRYLAIVHATR----------TLTQKRHLVKFVCLGCWGLSM 192
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Qy    228 LFALPDFIFLSAHHDERLNATHCQY----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYA 283
Db    193 NLSLPFFLFRQAYHPN--NSSPVCYEVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYG 250

Qy    284 HILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRV 343
Db    251 FTLRTLFKAHMGQKHRAMRVIFAVVLIFLLCWLPYNLVLLADTLMRTQVIQESCERRNNI 310

Qy    344 DVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSS 403
Db    311 GRALDATEILGFLHSCLNPIIYAFIGQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSS 370

Qy    404 WSETS 408
Db    371 VNVSS 375


RESULT 15
PCT-US02-15638-3
; Sequence 3, Application PC/TUS0215638
; GENERAL INFORMATION:
;  APPLICANT: Genaissance Pharmaceuticals, Inc.
;  APPLICANT:  Bieglecki, Karyn M.
;  APPLICANT:  Denton, R. Rex
;  APPLICANT:  Lee, Helen H.
;  APPLICANT:  Nandabalan, Krishnan
;  TITLE OF INVENTION: HAPLOTYPES OF THE IL8RA GENE
;  FILE REFERENCE: MWH-0441PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/15638
;  CURRENT FILING DATE:  2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,533
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Homo sapiens
PCT-US02-15638-3

  Query Match             28.2%;  Score 606.5;  DB 2;  Length 350;
  Best Local Similarity   39.7%;  Pred. No. 4.1e-43;
  Matches  135;  Conservative   50;  Mismatches  124;  Indels   31;  Gaps    5;

Qy     88 PPCPQDFS------LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLH 141
Db     21 PPADEDYSPCMLETETLNKYVVIIAYALVFLLSLLGNSLVMLVILYSRVGRSVTDVYLLN 80

Qy    142 LAVADTLLVLTLPLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIV 201
Db     81 LALADLLFALTLPIWAASKVNGWIFGTFLCKVVSLLKEVNFYSGILLLACISVDRYLAIV 140

Qy    202 HATQLYRRGPPARVTLT---------CLAVWGLCLLFALPDFIFLSAHHDERLNATHCQY 252
Db    141 HATR----------TLTQKRHLVKFVCLGCWGLSMNLSLPFFLFRQAYHPN--NSSPVCY 188

Qy    253 ----NFPQVGRTALRVLQLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVV 308
Db    189 EVLGNDTAKWRMVLRILPHTFGFIVPLFVMLFCYGFTLRTLFKAHMGQKHRAMRVIFAVV 248

Qy    309 VAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFV 368
Db    249 LIFLLCWLPYNLVLLADTLMRTQVIQESCERRNNIGRALDATEILGFLHSCLNPIIYAFI 308

Qy    369 GVKFRERMWMLLLRLGCPNQRGLQRQPSSSRRDSSWSETS 408
Db    309 GQNFRHGFLKILAMHGLVSKEFLARHRVTSYTSSSVNVSS 348


Search completed: November  2, 2002, 12:11:13
Job time : 126 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:20:26 ; Search time 1898 Seconds
(without alignments)
4575.613 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US09101518/runat_29102002_091101_24/app_query.fasta_1.583
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09101518_@CGN_1_1_1182_@runat_29102002_091101_24 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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12: gb_sy:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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21: em_or:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	2151	100.0	271144	9	HSXDPB	AL590763 Homo sapi
2	2146	99.8	1563	9	HSCKRL2	Z79783 H.sapiens G
3	2073	96.4	1293	9	HSU32674	U32674 Human orpha
4	1897	88.2	1670	6	AR117009	AR117009 Sequence
5	1897	88.2	1670	9	HSGPCRIN8	X95876 H.sapiens m
6	1644.5	76.5	1678	10	AF223642	AF223642 Rattus no
7	1632.5	75.9	1608	10	AB003174	AB003174 Mus muscu
8	1626.5	75.6	1525	10	AF045146	AF045146 Mus muscu
9	643	29.9	262652	2	AC105645	AC105645 Rattus no
10	641	29.8	1236	10	NRGPCNLR	X71463 R.norvegicu
11	640	29.8	2517	6	AR107998	AR107998 Sequence
12	640	29.8	2517	10	MMBLR1	X71788 M.musculus
13	637.5	29.6	2856	9	HUMIL8RB	L19593 Homo sapien
14	637.5	29.6	2856	11	G28560	G28560 human STS S
15	636	29.6	2847	9	HSIL8RB4	U11869 Human inter
16	636	29.6	13089	9	HUMIL8R	M99412 Human inter
17	635	29.5	1510	9	HUMINTLEU8	M73969 Human inter
18	635	29.5	1679	6	AR015971	AR015971 Sequence
19	635	29.5	1679	6	AR060749	AR060749 Sequence
20	635	29.5	1679	6	AR070434	AR070434 Sequence
21	635	29.5	1679	6	AR103431	AR103431 Sequence
22	635	29.5	1679	6	I13754	I13754 Sequence 6
23	635	29.5	1679	6	I24456	I24456 Sequence 5
24	635	29.5	1748	6	I13755	I13755 Sequence 8
25	635	29.5	1750	9	HUMILEU8R	M94582 Human inter
26	635	29.5	2818	6	AR107999	AR107999 Sequence
27	635	29.5	2818	6	AR151870	AR151870 Sequence
28	635	29.5	2818	9	HSBLR1A	X68149 Homo sapien
29	633.5	29.5	2020	9	HSMDCR	X68829 H.sapiens m
c 30	633.5	29.5	158634	2	AP000909	AP000909 Homo sapi
31	633	29.4	1068	23	E11245	E11245 Human cDNA
c 32	632.5	29.4	165394	2	AP000877	AP000877 Homo sapi
c 33	632.5	29.4	244847	2	AP002357	AP002357 Homo sapi
34	629.5	29.3	1060	9	MMMCIL8RB	X91116 M.mulatta M
35	628	29.2	3011	6	AX281745	AX281745 Sequence
36	622	28.9	1060	9	PTIL8RB	X91113 P.troglodyt
37	618.5	28.8	1122	9	MMIL8RA	X91112 M.mulatta M
38	615.5	28.6	1068	4	RABIL8C	M74240 Oryctolagus
39	615.5	28.6	1232	4	RABIL8REC	M82873 Oryctolagus
40	615	28.6	1206	4	RABIL8RSB	L24445 Oryctolagus
41	614.5	28.6	2245	9	HSHAIL8G	X65858 H.sapiens g
42	614.5	28.6	4452	9	HSU11870	U11870 Human inter
43	614.5	28.6	9269	9	HUMIL8RAB	L19592 Homo sapien
c 44	614.5	28.6	98433	9	AC097483	AC097483 Homo sapi
45	614	28.5	1060	9	GGIL8RB	X91114 G.gorilla G

ALIGNMENTS

RESULT 1
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LOCUS HSXDPB 271144 bp DNA linear PRI 17-JUN-2001
DEFINITION Homo sapiens chromosome X sequence from 6 PACs 1 BAC and 1 cosmid, region GJB1-DXS559 map Xq13.1, complete sequence.
ACCESSION AL590763 AJ239319
VERSION AL590763.1 GI:13751778
KEYWORDS HTG.
SOURCE human.

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 271144)
  AUTHORS   Ramser,J., Heitmann,K., Sudbrak,R., Kosiura,A., Klages,S.,
            Steffens,C., Borzym,K., Kube,M., Lehrack,S., Marquardt,I.,
            Schuelzchen,S., Starke,A., Thompson,C., Hennig,S., Francis,F.,
            Nemeth,A., Monaco,A., Lehrach,H. and Reinhardt,R.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 271144)
  AUTHORS   MPIMG.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-FEB-1999) MPIMG, Abt.Lehrach, Max Planck Institut
            Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
COMMENT     Bases 1. .5000 overlap with AL590762 (HSXDPA).
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                     /clone="PAC RPCI-1 2J13"
                     /clone="PAC RPCI-3 423F18"
                     /clone="PAC RPCI-1 104C1"
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                     /clone="BAC OX1"
                     /clone="PAC RPCI-1 56F19"
                     /clone_lib="RPCI1,3-5  Human PAC library, originating
                     institute: Roswell Park Cancer Institute, Creator: Pieter
                     de Jong, P. Ioannou"
                     /note="region between markers GJB1-DXS559"
BASE COUNT    71233 a  59391 c  63906 g  76614 t
ORIGIN

Alignment Scores:
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Score:                    2151.00        Matches:         415
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       9              Gaps:            0

US-09-101-518A-2 (1-415) x HSXDPB (1-271144)

Qy      1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
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Db 159068 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 159009

Qy     61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
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Db 159008 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 158949

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Db 158948 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 158889

Qy    101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
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Db 158888 GCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 158829

Qy    121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
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Qy    141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
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Qy    161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
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Db 158708 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 158649

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Db 158588 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 158529

Qy    221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
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Db 158528 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 158469

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGlnValGlyArgThr 260
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Db 158468 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 158409

Qy    261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
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Qy    301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
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Db 158288 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 158229

Qy    321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
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Db 158228 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 158169

Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
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Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
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Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
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Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
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Db 157988 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 157944

RESULT 2
HSCKRL2
LOCUS       HSCKRL2                 1563 bp    DNA     linear   PRI 26-JUL-1997
DEFINITION  H.sapiens G protein-coupled receptor CKR-L2.
ACCESSION   Z79783
VERSION     Z79783.1  GI:2281709
KEYWORDS    G Protein-coupled Receptor CKR-L2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1563)
  AUTHORS   Gutierrez,J., Varona,R., Zaballos,A., Lind,P. and Marquez,G.
  TITLE     unpublished
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1563)
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  AUTHORS   Zaballos,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) Angel Zaballos, Research, Pharmacia &
            Upjohn, Antonio Lopez 109, Madrid, 28026, Spain
FEATURES             Location/Qualifiers
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                     VMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDILMDLGALA
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BASE COUNT      272 a    497 c    479 g    315 t
ORIGIN

Alignment Scores:
Pred. No.:                5.77e-183      Length:          1563
Score:                    2146.00        Matches:         414
Percent Similarity:       99.76%         Conservative:    0
Best Local Similarity:    99.76%         Mismatches:      1
Query Match:              99.77%         Indels:          0
DB:                       9              Gaps:            0

US-09-101-518A-2 (1-415) x HSCKRL2 (1-1563)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
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Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
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Db     315 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 374

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
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Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
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Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
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Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
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Db     555 GCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 614

Qy     121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
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Qy     141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
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Qy     161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
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Qy     181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
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Qy     201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
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Db     855 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 914

Qy     221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
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Qy     241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGlnValGlyArgThr 260
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Qy     261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
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Qy     281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
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Qy     301 MetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
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Db    1155 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1214

Qy     321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
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Db    1215 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1274

Qy     341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
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Db    1275 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1334

Qy     361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
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Db    1335 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1394

Qy     381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
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Db    1395 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1454

Qy     401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
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Db    1455 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1499

RESULT 3
HSU32674
LOCUS       HSU32674                1293 bp    DNA     linear   PRI 05-JUN-1996
DEFINITION  Human orphan receptor GPR9 (GPR9) gene, partial cds.
ACCESSION   U32674
VERSION     U32674.1  GI:1002740
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1293)
  AUTHORS   Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
            Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
            and Docherty,J.M.
  TITLE     Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
            and GPR14, encoding receptors related to interleukin 8,
            neuropeptide Y, and somatostatin receptors
  JOURNAL   Genomics 29 (2), 335-344 (1995)
  MEDLINE   96115583
REFERENCE   2  (bases 1 to 1293)
  AUTHORS   Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
            Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
            and Docherty,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology,
            University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario M5S
```

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                     /translation="VSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFS
                     LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL
                     PLWAVDAAVQWVFGSGLCKVAGALFNINFYAGALLLACISFDRYLNIVHATQLYRRGP
                     PARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVA
                     GFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDIL
                     MDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGC
                     PNQRGLQRQPSSSRRDSSWSETSEASYSGL"
BASE COUNT      201 a    458 c    357 g    277 t
ORIGIN

Alignment Scores:
Pred. No.:              1.58e-176      Length:         1293
Score:                  2073.00        Matches:        400
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            96.37%         Indels:         0
DB:                     9              Gaps:           0

US-09-101-518A-2 (1-415) x HSU32674 (1-1293)

Qy      16 IleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPhe 35
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy      36 LeuProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy      56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAsp 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy      76 TyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy      96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy     116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy     136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy     156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy     176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy     196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy     216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy     236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy     256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy     276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy     296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy     316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy     336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy     356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy     376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy     396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

RESULT 4
AR117009
LOCUS       AR117009                1670 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6140064.
ACCESSION   AR117009
VERSION     AR117009.1  GI:14097915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1670)
  AUTHORS   Loetscher,M. and Moser,B.
  TITLE     Method of detecting or identifying ligands, inhibitors or promoters
            of CXC chemokine receptor 3
  JOURNAL   Patent: US 6140064-A 1 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1670
                     /organism="unknown"
BASE COUNT      272 a    574 c    436 g    388 t
ORIGIN

Alignment Scores:
Pred. No.:              1.29e-160      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
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Query Match:           88.19%      Indels:        4
DB:                    6           Gaps:          1

US-09-101-518A-2 (1-415) x AR117009 (1-1670)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||          ||||||          :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
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Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
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Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
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Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 5
HSGPCRIN8
LOCUS       HSGPCRIN8               1670 bp    mRNA    linear   PRI 16-MAY-1997
DEFINITION  H.sapiens mRNA for G-protein coupled receptor.
ACCESSION   X95876
VERSION     X95876.1  GI:1552845
KEYWORDS    G protein-coupled receptor; interleukin-8 receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1670)
  AUTHORS   Loetscher,M., Gerber,B., Loetscher,P., Jones,S.A., Piali,L.,
            Clark-Lewis,I., Baggiolini,M. and Moser,B.
  TITLE     Chemokine receptor specific for IP10 and mig: structure, function,
            and expression in activated T-lymphocytes
  JOURNAL   J. Exp. Med. 184 (3), 963-969 (1996)
  MEDLINE   97188912
REFERENCE   2  (bases 1 to 1670)
  AUTHORS   Loetscher,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-1996) M. Loetscher, Theodor-Kocher Institute,
            University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
FEATURES             Location/Qualifiers
     source          1. .1670
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                     /db_xref="taxon:9606"
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                     /haplotype="diploid"
                     /cell_line="KT30"
                     /cell_type="T lymphocytes CD4+"
                     /tissue_type="blood"
                     /clone_lib="lambda ZAP Express"
                     /dev_stage="adult"
     CDS             69. .1175
                     /codon_start=1
                     /product="G-protein coupled receptor"
                     /protein_id="CAA65126.1"
                     /db_xref="GI:1552846"
                     /db_xref="SWISS-PROT:P49682"
                     /translation="MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCP
                     QDFSLNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLL
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                     RRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVL
                     QLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVL
                     VDILMDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLL
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     polyA_signal    1602. .1607
     polyA_site      1623
BASE COUNT      319 a    574 c    436 g    341 t
ORIGIN

Alignment Scores:
Pred. No.:              1.29e-160      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     9              Gaps:           1

US-09-101-518A-2 (1-415) x HSGPCRIN8 (1-1670)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||          ||||||          :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95
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Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
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Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
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Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172
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RESULT 6
AF223642
LOCUS       AF223642               1678 bp    mRNA    linear   ROD 19-JUN-2000
DEFINITION  Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds.
ACCESSION   AF223642
VERSION     AF223642.1  GI:8572056
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1678)
  AUTHORS   Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S.
            and Sarau,H.M.
  TITLE     Identification and molecular characterization of rat CXCR3:
            receptor expression and interferon-inducible protein-10 binding are
            increased in focal stroke
  JOURNAL   Mol. Pharmacol. 57 (6), 1190-1198 (2000)
  MEDLINE   20286573
   PUBMED   10825390
REFERENCE   2  (bases 1 to 1678)
  AUTHORS   Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S.
            and Sarau,H.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-2000) Cardiovascular Sciences, DuPont
            Pharmaceuticals, Experimental Station E400/3420B, Wilmington, DE
            19880/0400, USA
FEATURES             Location/Qualifiers
     source          1. .1678
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /sex="male"
                     /note="spontaneously hypertensive"
     CDS             149. .1252
                     /codon_start=1
                     /product="chemokine receptor CXCR3"
                     /protein_id="AAF76982.1"
                     /db_xref="GI:8572057"
                     /translation="MYLEVSERQVLDASDIAFLLENSTSPYDYGENESDFSDSPPCPQ
                     DFSLNFDRTFLPVLYSLLFLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLV
                     LTLPLWAVDAAAQWVFGSGLCKVAGALFNINFYAGAFLLACISFDRYLSIVHATQIYR
                     RDPWVRVALTCIVVWGLCVLFALPDFIFLSASHDQRLNATHCQYNFPQVGRTALRVLQ
                     LVAGFLMPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVVAFAVCWTPYHLVVLV
                     DILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKFKEQMWMLLMR
                     LGRSDQRGPQRQPSSSRRESSWSETTEASYLGL"
BASE COUNT      370 a    486 c    417 g    405 t
ORIGIN

Alignment Scores:
Pred. No.:              5.52e-138      Length:         1678
Score:                  1644.50        Matches:        324
Percent Similarity:     86.24%         Conservative:   27
Best Local Similarity:  79.61%         Mismatches:     37
Query Match:            76.45%         Indels:         19
DB:                     10             Gaps:           3

US-09-101-518A-2 (1-415) x AF223642 (1-1678)

Qy       9 GlyArgLeuAlaGlyThrValIleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSer 28
           ||||||   ||||||:::                                  |||:::
Db      86 GGCAGAGAAGCAGGCAGC--------------------------------ACGAGACCT 112

Qy      29 AspSerIleThrLysGluPheLeuProGlyLeuTyrThrAlaProSerSerProPhePro 48
           |||                  |||      ::::::      ||||||
Db     113 GAC--------------------CCCAGCAGCCACAGCCAGAGCAGCAGCCAAGCCATG 151

Qy      49 ProSerGlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGlu 68
                ::::|||||:::   |||||||||:::   ::::::::::|||   |||||||||
Db     152 TACCTTGAGGTCAGTGAACGTCAAGTGCTAGATGCCTCGGACATTGCCTTTCTTCTGGAA 211

Qy      69 AsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerPro 88
           |||   :::|||   ||||||||||||||||||||||||||||            ||||||
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Db    212 AACAGCACATCTCCCTACGATTATGGGGAAAACGAAAGCGAC---TTCTCTGACTCCCCG 268

Qy     89 ProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSer 108
          ||||||||||||||||||||||||||||||||||   |||||||||   |||||||||
Db    269 CCCTGCCCACAGGACTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGTCCTCTACAGC 328

Qy    109 LeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArg 128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db    329 CTCCTCTTTTTGCTGGGGCTGCTAGGCAATGGGGCAGTGGCTGCTGTGCTACTGAGCCAG 388

Qy    129 ArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeu 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    389 CGCACTGCCCTGAGCAGCACAGACACCTTCCTGCTCCACCTGGCTGTGGCCGATGTACTG 448

Qy    149 LeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySer 168
          ||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db    449 CTGGTACTAACCCTCCCACTGTGGGCAGTAGATGCTGCTGCCCAGTGGGTTTTCGGCTCT 508

Qy    169 GlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeu 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    509 GGTCTCTGCAAAGTGGCAGGTGCCCTGTTCAACATCAACTTCTACGCAGGGGCCTTCCTG 568

Qy    189 LeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArg 208
          ||||||||||||||||||||||||||||:::|||||||||||||||||||:::||||||
Db    569 CTGGCCTGTATAAGCTTTGACCGCTACCTGAGCATAGTGCATGCCACCCAGATCTACCGC 628

Qy    209 ArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeu 228
          |||   |||       ||||||   |||||||||:::   ||||||||||||||:::|||
Db    629 AGGGACCCCTGGGTACGTGTAGCCCTCACCTGCATTGTTGTGTGGGGTCTCTGTGTGCTC 688

Qy    229 PheAlaLeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThr 248
          ||||||||||||||||||||||||||||||   ||||||:::||||||||||||||||||
Db    689 TTTGCCCTCCCAGATTTCATCTTCCTGTCAGCCAGCCATGATCAGCGCCTCAATGCCACC 748

Qy    249 HisCysGlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuVal 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    749 CATTGCCAGTACAACTTCCCACAGGTGGGTCGGACTGCTCTGCGTGTACTGCAGCTAGTG 808

Qy    269 AlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaVal 288
          ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db    809 GCTGGTTTCCTGATGCCCCTTCTAGTCATGGCCTACTGCTATGCCCATATCCTGGCTGTG 868

Qy    289 LeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValVal 308
          ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db    869 CTGCTGGTCTCCAGAGGCCAGAGGCGCTTTCGAGCTATGAGGCTAGTGGTGGTGGTGGTG 928

Qy    309 ValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMet 328
          ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db    929 GTGGCCTTTGCCGTCTGCTGGACCCCCTATCACCTGGTGGTGTTAGTGGATATCCTTATG 988

Qy    329 AspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSer 348
          |||:::|||   |||||||||||||||||||||||||   |||||||||||||||||||
Db    989 GACGTGGGAGTTTTGGCCCGCAACTGTGGTCGAGAAAGCCATGTGGACGTAGCCAAGTCA 1048

Qy    349 ValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheVal 368
          ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   1049 GTCACCTCAGGCATGGGCTACATGCACTGCTGCCTCAATCCACTGCTCTATGCCTTTGTG 1108

Qy    369 GlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGln 388
          ||||||||||||:::|||:::|||||||||||||||||:::|||||||||      :::|||
Db   1109 GGAGTGAAGTTCAAAGAACAAATGTGGATGTTGCTCATGCGCCTGGGCCGCTCTGACCAG 1168

Qy    389 ArgGlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
          ||||||   ||||||||||||||||||||||||||:::||||||||||||||||||:::
Db   1169 AGAGGACCGCAGCGGCAGCCTTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACT 1228

Qy    409 GluAlaSerTyrSerGlyLeu 415
          ||||||||||||   ||||||
Db   1229 GAGGCCTCCTACTTGGGCTTG 1249

RESULT 7
AB003174
LOCUS       AB003174               1608 bp    mRNA    linear   ROD 28-OCT-1998
DEFINITION  Mus musculus mRNA for interferon-inducible protein 10 receptor,
            complete cds.
ACCESSION   AB003174
VERSION     AB003174.1  GI:3798731
KEYWORDS    interferon-inducible protein 10 receptor.
SOURCE      Mus musculus blood cytotoxic T cells cell_line:CTLL-2 cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1608)
  AUTHORS   Tamaru,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-1997) Masahiro Tamaru, Japan Tobacco Inc. Central
            Pharmaceutical Reseach Institute, Pharmaceutical Frontier Reseach
            Laboratories; 13-2, Fukuura 1-chome, Kanazawa-ku, Yokohama,
            Kanagawa 236, Japan (E-mail:tamaru@ikrl.jti.co.jp,
            Tel:81-45-786-7694, Fax:81-45-786-7692)
REFERENCE   2  (sites)
  AUTHORS   Tamaru,M., Tominaga,Y., Yatsunami,K. and Narumi,S.
  TITLE     Cloning of the murine interferon-inducible protein 10 (IP-10)
            receptor and its specific expression in lymphoid organs
  JOURNAL   Biochem. Biophys. Res. Commun. 251 (1), 41-48 (1998)
  MEDLINE   99009219
FEATURES             Location/Qualifiers
     source          1. .1608
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                     /cell_line="CTLL-2"
                     /cell_type="cytotoxic T cells"
                     /tissue_type="blood"
     gene            90. .1193
                     /gene="MCXCR3"
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                     /gene="MCXCR3"
                     /codon_start=1
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                     /protein_id="BAA34045.1"
                     /db_xref="GI:3798732"
                     /translation="MYLEVSERQVLDASDFAFLLENSTSPYDYGENESDFSDSPPCPQ
                     DFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLV
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                     RDPRVRVALTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQ
                     LVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLV
                     DILMDVGVLARNCGRESHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKFREQMWMLFTR
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     polyA_site      1608
                     /note="51 a nucleotides"
BASE COUNT      338 a    469 c    409 g    392 t
ORIGIN

Alignment Scores:
Pred. No.:              6.22e-137      Length:          1608
Score:                  1632.50        Matches:         323
Percent Similarity:     85.75%         Conservative:    26
Best Local Similarity:  79.36%         Mismatches:      39
Query Match:            75.89%         Indels:          19
DB:                     10             Gaps:            3

US-09-101-518A-2 (1-415) x AB003174 (1-1608)

Qy      9 GlyArgLeuAlaGlyThrValIleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSer 28
          ||||||   ||||||:::                                    |||:::
Db     27 GGCAGAGAAGCAGGCAGC------------------------------ACGAGACCT 53

Qy     29 AspSerIleThrLysGluPheLeuProGlyLeuTyrThrAlaProSerSerProPhePro 48
          |||                    |||      ::::::      :::|||
Db     54 GAC-------------------CCCAGCAGCCACAGCCGGAGCACCAGCCAAGCCATG 92

Qy     49 ProSerGlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGlu 68
             :::|||||||:::   ||||||||||:::   ::::::   |||   |||||||||
Db     93 TACCTTGAGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAA 152

Qy     69 AsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerPro 88
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          |||   :::|||   |||||||||||||||||||||||||||           ||||||
Db    153 AACAGCACCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCG 209

Qy     89 ProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSer 108
          ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db    210 CCCTGCCCACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGC 269

Qy    109 LeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArg 128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db    270 CTCCTCTTCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAG 329

Qy    129 ArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeu 148
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Db    330 CGCACTGCCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTG 389

Qy    149 LeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySer 168
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Db    390 CTGGTGTTAACTCTTCCATTGTGGGCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCT 449

Qy    169 GlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeu 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db    450 GGCCTCTGCAAAGTGGCAGGCGCCTTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTG 509

Qy    189 LeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArg 208
          ||||||||||||||||||||||||||||:::|||||||||||||||||:::||||||
Db    510 CTGGCTTGTATAAGCTTCGACAGATATCTGAGCATAGTGCACGCCACCCAGATCTACCGC 569

Qy    209 ArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeu 228
          |||   |||      ||||||   |||||||||:::   ||||||||||||||||||||
Db    570 AGGGACCCCCGGGTACGTGTAGCCCTCACCTGCATAGTTGTATGGGGTCTCTGTCTGCTC 629

Qy    229 PheAlaLeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThr 248
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Db    630 TTTGCCCTCCCAGATTTCATCTACCTATCAGCCAACTACGATCAGCGCCTCAATGCCACC 689

Qy    249 HisCysGlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuVal 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 CATTGCCAGTACAACTTCCCACAGGTGGGTCGCACTGCTCTGCGTGTACTGCAGCTAGTG 749

Qy    269 AlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaVal 288
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Db    750 GCTGGTTTCCTGCTGCCCCTTCTGGTCATGGCCTACTGCTATGCCCATATCCTAGCTGTT 809

Qy    289 LeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValVal 308
          ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db    810 CTGCTGGTCTCCAGAGGCCAGAGGCGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTG 869

Qy    309 ValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMet 328
             |||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db    870 GCAGCCTTTGCTGTCTGCTGGACCCCCTATCACCTGGTGGTGCTAGTGGATATCCTCATG 929

Qy    329 AspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSer 348
          |||:::|||   ||||||||||||||||||||||||||   ||||||||||||||||||
Db    930 GATGTGGGAGTTTTGGCCCGCAACTGTGGTCGAGAAAGCCACGTGGATGTGGCCAAGTCA 989

Qy    349 ValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheVal 368
          ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db    990 GTCACCTCGGGCATGGGGTACATGCACTGCTGCCTCAATCCGCTGCTCTATGCCTTTGTG 1049

Qy    369 GlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGln 388
          ||||||||||||||||||:::|||||||||||||      |||||||||      :::|||
Db   1050 GGAGTGAAGTTCAGAGAGCAAATGTGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAG 1109

Qy    389 ArgGlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
          ||||||   |||||||||||||||||||||||||||:::||||||||||||||||||:::
Db   1110 AGAGGGCCCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACT 1169

Qy    409 GluAlaSerTyrSerGlyLeu 415
          |||||||||||||   ||||||
Db   1170 GAGGCCTCCTACCTGGGCTTG 1190

RESULT 8
AF045146
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LOCUS       AF045146               1525 bp    mRNA    linear   ROD 10-JUL-1998
DEFINITION  Mus musculus chemokine receptor CXCR3 mRNA, complete cds.
ACCESSION   AF045146
VERSION     AF045146.1  GI:3282809
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1525)
  AUTHORS   Soto,H., Wang,W., Strieter,R.M., Copeland,N.G., Gilbert,D.J.,
            Jenkins,N.A., Hedrick,J. and Zlotnik,A.
  TITLE     The CC chemokine 6Ckine binds the CXC chemokine receptor CXCR3
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (14), 8205-8210 (1998)
  MEDLINE   98318636
REFERENCE   2  (bases 1 to 1525)
  AUTHORS   Soto,H. and Zlotnik,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-1998) Immunobiology, DNAX Research Institute, 901
            California Ave., Palo Alto, CA 94304, USA
FEATURES             Location/Qualifiers
     source          1. .1525
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                     /protein_id="AAC40163.1"
                     /db_xref="GI:3282810"
                     /translation="MYLEVSERQVLDASDFAFLLENSTSPYDYGENESDFSDSPPCPQ
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                     RDPRVRVALTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQ
                     LVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLV
                     DILMDVGVLARNCGRKSHVDVAKSVTSGMGYMHCCLNPLLYAFVGVKFREKMWMLFTR
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BASE COUNT      316 a    433 c    386 g    390 t
ORIGIN

Alignment Scores:
Pred. No.:              2.01e-136      Length:          1525
Score:                  1626.50        Matches:         314
Percent Similarity:     92.05%         Conservative:    22
Best Local Similarity:  86.03%         Mismatches:      28
Query Match:            75.62%         Indels:          1
DB:                     10             Gaps:            1

US-09-101-518A-2 (1-415) x AF045146 (1-1525)

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Db     10 GAGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGC 69

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
          :::|||   ||||||||||||||||||||||||||           ||||||||||||
Db     70 ACCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGC 126

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db    127 CCACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTC 186

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    187 TTCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACT 246

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
          ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    247 GCCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTG 306

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    307 TTAACTCTTCCATTGTGGGCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCTGGCCTC 366
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Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    367 TGCAAAGTGGCAGGCGCCTTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTGCTGGCT 426

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
          ||||||||||||||||||||||:::|||||||||||||||||||:::|||||||||
Db    427 TGTATAAGCTTCGACAGATATCTGAGCATAGTGCACGCCACCCAGATCTACCGCAGGGAC 486

Qy    211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
          |||      ||||||   |||||||||:::   ||||||||||||||||||||||||||
Db    487 CCCCGGGTACGTGTAGCCCTCACCTGCATAGTTGTATGGGGTCTCTGTCTGCTCTTTGCC 546

Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
          ||||||||||||||:::|||||||||:::::::|||:::|||||||||||||||||||||
Db    547 CTCCCAGATTTCATCTACCTATCAGCCAACTACGATCAGCGCCTCAATGCCACCCATTGC 606

Qy    251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 CAGTACAACTTCCCACAGGTGGGTCGCACTGCTCTGCGTGTACTGCAGCTAGTGGCTGGT 666

Qy    271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 TTCCTGCTGCCCCTTCTGGTCATGGCCTACTGCTATGCCCATATCCTAGCTGTTCTGCTG 726

Qy    291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
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Db    727 GTCTCCAGAGGCCAGAGGCGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTGGCAGCC 786

Qy    311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
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Db    787 TTTGCTGTCTGCTGGACCCCCTATCACCTGGTGGTGCTAGTGGATATCCTCATGGATGTG 846

Qy    331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
          |||   ||||||||||||||||||:::|||   ||||||||||||||||||||||||||
Db    847 GGAGTTTTGGCCCGCAACTGTGGTCGAAAAAGCCACGTGGATGTGGCCAAGTCAGTCACC 906

Qy    351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
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Db    907 TCGGGCATGGGGTACATGCACTGCTGCCTCAATCCGCTGCTCTATGCCTTTGTGGGAGTG 966

Qy    371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
          ||||||||||||:::|||||||||||||      |||||||||      :::|||||||||
Db    967 AAGTTCAGAGAGAAAATGTGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAGAGAGGG 1026

Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
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Db   1027 CCCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCC 1086

Qy    411 SerTyrSerGlyLeu 415
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Db   1087 TCCTACCTGGGCTTG 1101
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RESULT 9
AC105645
LOCUS       AC105645               262652 bp    DNA     linear   HTG 09-JAN-2002
DEFINITION  Rattus norvegicus chromosome Iddm4 clone CH230-205K13, WORKING
            DRAFT SEQUENCE, 75 unordered pieces.
ACCESSION   AC105645
VERSION     AC105645.1  GI:18092868
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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REFERENCE   1  (bases 1 to 262652)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 262652)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
               Center: Baylor College of Medicine
               Center code: BCM
               Web site: http://www.hgsc.bcm.tmc.edu/
               Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
               Center project name: GNKV
               Center clone name: CH230-205K13
            -------------- Summary Statistics
               Assembly program: Phrap; version 0.990329First call to
            findPhrapList
               Consensus quality: 230579 bases at least Q40
               Consensus quality: 238922 bases at least Q30
               Consensus quality: 245707 bases at least Q20
               Estimated insert size: 234543; sum-of-contigs estimation
               Quality coverage: 0x in Q20 bases; agarose-fp estimation
               Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length .
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 75 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    15232: contig of 15232 bp in length
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            *    15333    27159: contig of 11827 bp in length
            *    27160    27259: gap of unknown length
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*    27260    36908: contig of 9649 bp in length
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*    46033    46132: gap of unknown length
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*    55882    55981: gap of unknown length
*    55982    63023: contig of 7042 bp in length
*    63024    63123: gap of unknown length
*    63124    71683: contig of 8560 bp in length
*    71684    71783: gap of unknown length
*    71784    78964: contig of 7181 bp in length
*    78965    79064: gap of unknown length
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*    85068    85167: gap of unknown length
*    85168    91046: contig of 5879 bp in length
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*    96567    96666: gap of unknown length
*    96667   102141: contig of 5475 bp in length
*   102142   102241: gap of unknown length
*   102242   106671: contig of 4430 bp in length
*   106672   106771: gap of unknown length
*   106772   112153: contig of 5382 bp in length
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*   145095   148532: contig of 3438 bp in length
*   148533   148632: gap of unknown length
*   148633   151786: contig of 3154 bp in length
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*   151887   157150: contig of 5264 bp in length
*   157151   157250: gap of unknown length
*   157251   161920: contig of 4670 bp in length
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*   162021   165493: contig of 3473 bp in length
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*   168208   168307: gap of unknown length
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*   171753   171852: gap of unknown length
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*   173964   174063: gap of unknown length
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*   196724   196823: gap of unknown length
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*   198734   198833: gap of unknown length
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*   200711   200810: gap of unknown length
*   200811   202176: contig of 1366 bp in length
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Alignment Scores:
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Percent Similarity:     55.00%          Conservative:   48
Best Local Similarity:  41.67%          Mismatches:     142
Query Match:            29.89%          Indels:         20
DB:                     2               Gaps:           7

US-09-101-518A-2 (1-415) x AC105645 (1-262652)

Qy      69 AsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerPro 88
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Db   38432 TCTTTCTCTTTGTCCTTGCAGTACAAGGAACTGGCCATCTACAGTAACAGCACGGAGATC 38491

Qy      89 Pro-----------------CysProGlnAsp---------PheSerLeuAsnPheAsp 99
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Db   38552 ACGATATTCATGCCTGTGGCCTACAGCCTCATCTTCCTCCTGGGTATGATGGGAAACATC 38611

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Db   38612 CTCGTACTGGTAATCCTGGAGAGGCACCGGCACACTCGGAGCTCAACGGAGACCTTCCTG 38671

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
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Db  38852 ATCGTCCATGCGGTCCACGCCTACCGCCGCCGCCGTCTCCTCTCCATCCACATCACCTGC 38911

Qy    220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe--------- 236
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Db  38912 TCGACTATTTGGCTAGCCGGCTTCCTATTTGCCTTGCCAGAACTCCTCTTTGCCAAGGTT 38971

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
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Db  38972 GTCCAACCTCATAACAACGAGTCCTTA------CCACAGTGCATCTTCTCCCAAGAAAAT 39025

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Db  39026 GAAGCCGAAACTAGAGCCTGGTTCGCCTCCCGGTTTCTCTACCACACTGGGGGCTTCCTG 39085

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Db  39086 CTACCGATGCTCGTGATGGCCTGGTGTTATGTGGGAGTGGTACACAGGCTATTGCAGGCC 39145

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Qy    372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
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RESULT 10
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LOCUS       NRGPCNLR                1236 bp    DNA     linear   ROD 13-DEC-1994
DEFINITION  R.norvegicus m RNA for G-Protein-coupled receptor (NLR).
ACCESSION   X71463 S59748
VERSION     X71463.1  GI:599926
KEYWORDS    G-protein coupled receptor; NLR gene.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
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            Rattus.
REFERENCE   1  (bases 1 to 1236)
  AUTHORS   Kouba,M., Vanetti,M., Wang,X., Schafer,M. and Hollt,V.
  TITLE     Cloning of a novel putative G-protein-coupled receptor (NLR) which
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  JOURNAL   FEBS Lett. 321 (2-3), 173-178 (1993)
  MEDLINE   93238948
REFERENCE   2  (bases 1 to 1236)
  AUTHORS   Kouba,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-1993) M. Kouba, Dept. of Physiology, Univ. of
            Munich, Pettendoferstrasse 12, D-8000 Muenchen 2, FRG
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                     YHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLNPMLYTFAGVKFRSD
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     exon            58. .1125
                     /gene="rNLR"
                     /number=2
BASE COUNT      241 a    374 c    300 g    321 t
ORIGIN

Alignment Scores:
Pred. No.:                3.16e-48        Length:          1236
Score:                    641.00          Matches:         146
Percent Similarity:       56.00%          Conservative:    50
Best Local Similarity:    41.71%          Mismatches:      140
Query Match:              29.80%          Indels:          14
DB:                       10              Gaps:            6

US-09-101-518A-2 (1-415) x NRGPCNLR (1-1236)

Qy     70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
          :::|||:::|||   :::            :::|||      |||   |||
Db     76 TACAGTAACAGCACGGAGATCCCCCTACAGGACAGTATCTTCTGTTCTACAGAG------ 129

Qy     90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                              :::|||        |||:::|||      |||||||||
Db    130 ---GAGGGGCCCCTACTGACTTCCTTTAAGACGATATTCATGCCTGTGGCCTACAGCCTC 186

Qy    110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
          :::|||||||||||||:::::::||||||      |||      :::|||         |||
Db    187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTCGTACTGGTAATCCTGGAGAGGCACCGG 246

Qy    130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
                   ||||||||||:::|||||||||   ||||||||||||||||||   ||||||
Db    247 CACACTCGGAGCTCAACGGAGACCTTCCTGTTCCACCTGGCAGTAGCCGACCTTCTCTTG 306

Qy    150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
          |||      ||||||          :::   :::|||   ||||||   |||:::
Db    307 GTCTTCATCTTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy    170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
          |||||||||         ||||||      ||||||||||||      :::|||||||||
Db    367 CTCTGCAAAACTGTGATCGCCCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTGCTG 426

Qy    190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
          ||||||||:::   ||||||||||||   ||||||||||||          |||||||||
Db    427 GCCTGCATAGCTGTCGACCGTTATCTGGCCATCGTCCATGCGGTCCACGCCTACCGCCGC 486

Qy    210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                   :::   :::||||||      :::|||          ||||||
Db    487 CGCCGTCTCCTCTCTATCCACATCACCTGCTCGACTATTTGGCTAGCCGGCTTCCTATTT 546
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Qy    230 AlaLeuProAspPheIlePhe---------LeuSerAlaHisHisAspGluArgLeuAsn 246
          |||||||||:::   :::|||         :::      |||:::::::|||   |||
Db    547 GCCTTGCCAGAACTCCTCTTTGCCAAGGTTGTCCAACCTCATAACAACGAGTCCTTA--- 603

Qy    247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr-----------AlaLeu 262
              |||   ::::::                |||           |||
Db    604 ---CCACAGTGCATCTTCTCCCAAGAAAATGAAGCCGAAACTAGAGCCTGGTTCGCCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
          |||   |||           ||||||||||||||:::||||||||||||:::||||||
Db    661 CGGTTTCTCTACCACACTGGGGGCTTCCTGCTACCGATGCTCGTGATGGCCTGGTGTTAT 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
              ::::::      ||||||         |||      :::|||   :::|||:::
Db    721 GTGGGAGTGGTACACAGGCTATTGCAGGCCCAGCGGCGCCCTCAGAGGCAGAAGGCAGTC 780

Qy    302 ArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
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Db    781 AGGGTGGCCATCTTGGTGACAAGCATCTTCCTTCTCTGCTGGTCACCCTACCACATTGTC 840

Qy    322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
          :::   :::|||   |||      |||   |||:::      :::|||
Db    841 ATCTTCCTCGATACACTGGAAAGGCTGAAGGCTGTGAACAGCAGTTGCGAATTGAGTGGC 900

Qy    342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
             :::   ||||||   ::::::         ||||||      ||||||||||||||
Db    901 TACCTCTCAGTGGCTATCACCTTATGTGAATTCCTGGGCCTGGCTCACTGCTGTCTCAAT 960

Qy    362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
          |||:::||||||   |||   |||||||||||||      :::      ||||||
Db    961 CCCATGCTCTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACTTGTCTCGGCTTCTGACC 1020

Qy    382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
          :::||||||||||         |||      |||         |||
Db   1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGTCAGCTCTTTCCGGGCTGGCGCAAG 1077

Qy    402 SerSerTrpSerGluThrSerGluAlaSer 411
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Db   1078 AGCAGTCTCTCTGAGTCAGAGAACGCTACT 1107

RESULT 11
AR107998
LOCUS       AR107998               2517 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6110695.
ACCESSION   AR107998
VERSION     AR107998.1  GI:12823485
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2517)
  AUTHORS   Gunn,M.Dee, Williams,L.T. and Cyster,J.G.
  TITLE     Modulating the interaction of the chemokine, B Lymphocyte
            Hemoattractant, and its Receptor, BLR1
  JOURNAL   Patent: US 6110695-A 5 29-AUG-2000;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      620 a    727 c    601 g    569 t
ORIGIN

Alignment Scores:
Pred. No.:              9.64e-48        Length:         2517
Score:                  640.00          Matches:        143
Percent Similarity:     56.29%          Conservative:   54
Best Local Similarity:  40.86%          Mismatches:     139
Query Match:            29.75%          Indels:         14
DB:                     6               Gaps:           6

US-09-101-518A-2 (1-415) x AR107998 (1-2517)

Qy     70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
          :::|||:::|||   :::           :::|||:::   |||   |||
Db     76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy     90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                                 :::|||         |||:::|||      |||||||||
Db    127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186

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Db    187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy    130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
               |||||||||:::|||||||||   ||||||||||||||||||   ||||||
Db    247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy    150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
          |||      ||||||           :::   :::|||   ||||||   |||:::
Db    307 GTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy    170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
          |||||||||         ||||||      ||||||||||||      :::||||||:::
Db    367 CTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTCGTG 426

Qy    190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
          |||||||||:::   ||||||||||||   ||||||||||||              ||||||||
Db    427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy    210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                         :::   :::||||||   |||:::|||                |||||
Db    487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy    230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
          |||||||||:::   :::|||                  |||::::::::::   |||
Db    547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

Qy    247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr-----------AlaLeu 262
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Db    604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
          |||   |||      :::   |||||||||||||||:::|||||||||   :::||||||
Db    661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
              ::::::      ||||||         |||      :::|||   :::|||:::
Db    721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy    302 ArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
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Db    781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840

Qy    322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
          :::   :::|||   |||      |||   |||:::      :::|||
Db    841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy    342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
             :::   ||||||   ::::::         ||||||      ||||||||||||||
Db    901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy    362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
          |||:::||||||   |||   |||||||||||||      :::      ||||||
Db    961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy    382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
          :::||||||||||         |||      |||         :::   |||
Db   1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy    402 SerSerTrpSerGluThrSerGluAlaSer 411
          ||||||   ||||||:::      |||:::
Db   1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107

RESULT 12
MMBLR1
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LOCUS       MMBLR1                  2517 bp    mRNA    linear   ROD 06-NOV-1997
DEFINITION  M.musculus blr-1 gene for Burkitt lymphoma receptor 1 homologue.
ACCESSION   X71788
VERSION     X71788.1  GI:2598563
KEYWORDS    blr1 gene; G-protein coupled receptor; glycoprotein; transmembrane.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2517)
  AUTHORS   Kaiser,E., Forster,R., Wolf,I., Ebensperger,C., Kuehl,W.M. and
            Lipp,M.
  TITLE     The G protein-coupled receptor BLR1 is involved in murine B cell
            differentiation and is also expressed in neuronal tissues
  JOURNAL   Eur. J. Immunol. 23 (10), 2532-2539 (1993)
  MEDLINE   94009211
REFERENCE   2  (bases 1 to 2517)
  AUTHORS   Lipp,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAY-1993) M. Lipp, Inst. f. Biochemie der Univ.
            Muenchen, Am Klopferspitz 18a, D-82152 Martinsried, FRG
COMMENT     On Nov 9, 1997 this sequence version replaced gi:433946.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
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                     /dev_stage="adult"
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                     /gene="blr-1"
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                     RRRRLLSIHITCTAIWLAGFLFALPELLFAKVGQPHNNDSLPQCTFSQENEAETRAWF
                     TSRFLYHIGGFLLPMLVMGWCYVGVVHRLLQAQRRPQRQKAVRVAILVTSIFFLCWSP
                     YHIVIFLDTLERLKAVNSSCELSGYLSVAITLCEFLGLAHCCLNPMLYTFAGVKFRSD
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                     /number=4
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BASE COUNT      620 a    727 c    601 g    569 t
ORIGIN
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Alignment Scores:

Pred. No.:	9.64e-48	Length:	2517
Score:	640.00	Matches:	143
Percent Similarity:	56.29%	Conservative:	54
Best Local Similarity:	40.86%	Mismatches:	139
Query Match:	29.75%	Indels:	14
DB:	10	Gaps:	6

US-09-101-518A-2 (1-415) x MMBLR1 (1-2517)

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Qy     70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
          :::|||:::|||   :::          :::|||:::   |||   |||
Db     76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy     90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                              :::|||         |||:::|||      |||||||||
Db    127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186

Qy    110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
          :::||||||||||||:::::||||||      |||      :::|||         |||
Db    187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy    130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
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Db    247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy    150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
          |||      ||||||           :::   :::|||   ||||||   |||:::
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Qy    190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
          ||||||||||:::   ||||||||||||   ||||||||||||      |||||||||
Db    427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy    210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                    :::   :::||||||   |||:::|||            ||||||
Db    487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy    230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
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Db    547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

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Db    604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
          |||   |||      :::   ||||||||||||||||:::|||||||||   :::||||||
Db    661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
                ::::::      ||||||         |||      :::|||   :::|||:::
Db    721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy    302 ArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
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Db    781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840
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Qy     322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
           :::   :::|||   |||      |||   |||:::      :::|||
Db     841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy     342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
             :::   ||||||   ::::::        ||||||      ||||||||||||||||
Db     901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy     362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
           |||:::||||||   |||   ||||||||||||||      :::      ||||||
Db     961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy     382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
           :::||||||||||               |||      |||         :::   |||
Db    1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy     402 SerSerTrpSerGluThrSerGluAlaSer 411
           ||||||   ||||||:::      |||:::
Db    1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107
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RESULT 13
HUMIL8RB
LOCUS       HUMIL8RB               2856 bp    mRNA    linear   PRI 06-JAN-1995
DEFINITION  Homo sapiens interleukin 8 receptor beta (IL8RB) mRNA, complete
            cds.
ACCESSION   L19593
VERSION     L19593.1  GI:559053
KEYWORDS    interleukin 8 receptor beta.
SOURCE      Homo sapiens (tissue library: lanbda-DASH) cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2856)
  AUTHORS   Murphy,P.M. and Tiffany,H.L.
  TITLE     Cloning of complementary DNA encoding a functional human
            interleukin-8 receptor
  JOURNAL   Science 253 (5025), 1280-1283 (1991)
  MEDLINE   91368200
REFERENCE   2  (bases 1 to 2856)
  AUTHORS   Sprenger,H., Lloyd,A.R., Lautens,L.L., Bonner,T.I. and Kelvin,D.J.
  TITLE     Structure, genomic organization and expression of the human
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  JOURNAL   J. Biol. Chem. (1994) In press
FEATURES             Location/Qualifiers
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Percent Similarity:     51.09%         Conservative:    57
Best Local Similarity:  37.29%         Mismatches:      145
Query Match:            29.64%         Indels:          57
DB:                     9              Gaps:            10

US-09-101-518A-2 (1-415) x HUMIL8RB (1-2856)

Qy      17 GlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeu 36
           ||||||      |||   ||||||
Db     349 GGAGGTGTCCTACAGGTGAAAAGC---------------------------------- 372

Qy      37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55
                   |||      |||   |||         |||::::::   |||
Db     373 ------------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT 420

Qy      56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe--------------- 70
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Db     421 AACATGGAGAGTGACAGC--------------TTTGAAGATTTCTGGAAAGGTGAAGAT 465

Qy      71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
              |||:::|||   |||                              :::   ||||||
Db     466 CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT 525

Qy      91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
                ::   ||||||      ::::::   |||:::      :::|||:::|||:::
Db     526 GAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA 582

Qy     111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
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Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
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Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
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          |||||||||   ||||||||||||   ||||||||||||||:::
Db    823 TGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC-------------- 867

Qy    211 ProProAlaArgValThrLeuThr--------------------------CysLeuAla 221
                      ||||||||                              ||||||:::
Db    868 --------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGC 912

Qy    222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241
          :::||||||||||   ||||||   |||||||||      :::|||           :::
Db    913 ATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTAC 972

Qy    242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly--------- 258
                ::::::         |||         :::      :::|||
Db    973 TCATCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACA 1020

Qy    259 ---------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
                  |||      ||||||:::|||             ||||||::::::||||||
Db   1021 GCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTG 1080

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
          |||:::|||   :::||||||         |||      |||      :::
Db   1081 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG 1140

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
          ::::::   ||||||||||||::::::      ||||||:::   |||   ||||||||
Db   1141 CAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTCTGCTGG 1200

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
             ||||||:::||||||:::|||   |||   ||||||              :::
Db   1201 CTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG 1260

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
             |||   |||   :::   :::|||   |||         |||      ||||||
Db   1261 ACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATC 1320

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
          :::|||   ||||||||||||||:::|||||||||:::|||   |||||||||
Db   1321 CTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGA 1380

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          :::      :::|||       |||      ::::::     |||   :::
Db   1381 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC 1440

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
                |||         ||||||         ||||||
Db   1441 AGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1479

RESULT 14
G28560
LOCUS       G28560                  2856 bp    DNA     linear   STS 11-JUL-1996
DEFINITION  human STS SHGC-35278, sequence tagged site.
ACCESSION   G28560
VERSION     G28560.1  GI:1408375
KEYWORDS    STS; STS sequence; primer; sequence tagged site.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2856)
  AUTHORS   Myers,R.M.
  JOURNAL   Unpublished
COMMENT
            Contact: Richard M. Myers
            Stanford Human Genome Center (SHGC)
            Stanford University School of Medicine
            Department of Genetics, M-344, Stanford, CA 94305, USA
            Tel: 4157259687
            Fax: 4157259689
            Email: myers@shgc.stanford.edu

            Primer A: ACATTCCAAGCCTCATGTCC
            Primer B: CTTAGAACATAGAGTGCCATGGG
            STS size: 217
            PCR Profile:
                    Initial incubation: 94 degrees C for 90 seconds

                    Denaturation:       94 degrees C for 15 seconds
                    Annealing:          62 degrees C for 23 seconds
                    Polymerization:     72 degrees C for 30 seconds
                    PCR Cycles:         30
                    Thermal Cycler:     Perkin Elmer 9600
            Protocol:
                    Template:       25 ng
                    Primer:         each 1 uM
                    dNTPs:          each 200 uM
                    Taq Polymerase: 0.05 units/ul
                    Total Vol:      10 ul

            Buffer:
                    MgCl2:          2.5 mM
                    KCl:            50  mM
                    Tris-HCl:       20  mM
                    pH:             8.3

            Prepared with primer pairs provided by Sandoz, derived from L19593
            -- Washington University/Merck EST sequence.
FEATURES             Location/Qualifiers
     source          1. .2856
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="2"
     STS             1543. .1759
     primer_bind     1543. .1562
     primer_bind     complement(1737. .1759)
BASE COUNT      755 a    729 c    636 g  . 736 t
ORIGIN

Alignment Scores:
Pred. No.:              1.9e-47       Length:         2856
Score:                  637.50        Matches:        154
Percent Similarity:     51.09%        Conservative:   57
Best Local Similarity:  37.29%        Mismatches:     145
Query Match:            29.64%        Indels:         57
DB:                     11            Gaps:           10

US-09-101-518A-2 (1-415) x G28560 (1-2856)

Qy     17 GlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeu 36
          ||||||      |||   ||||||
Db    349 GGAGGTGTCCTACAGGTGAAAAGC---------------------------------- 372

Qy     37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55
                        |||      |||   |||         |||::::::   |||
Db    373 -----------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT 420

Qy     56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe--------------- 70
             :::   :::|||:::                  |||:::|||
Db    421 AACATGGAGAGTGACAGC--------------TTTGAAGATTTCTGGAAAGGTGAAGAT 465

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
             |||::|||   |||                                 :::   ||||||
Db    466 CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT 525

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
                :::   ||||||      ::::::   |||:::      :::|||:::|||:::
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Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
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Db    583 TTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTC 642

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
              |||   ||||||   :::||||||:::||||||:::||||||   |||
Db    643 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC 702

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||||||||:::||||||                |||:::||||||:::   |||
Db    703 CTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTG 762

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          ||||||||         |||      :::|||||||||:::|||   ||||||||||||
Db    763 TGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCC 822

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
          ||||||||   ||||||||||||   ||||||||||||||:::
Db    823 TGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC--------------- 867

Qy    211 ProProAlaArgValThrLeuThr---------------------------CysLeuAla 221
                        |||||||||                           ||||||:::
Db    868 --------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGC 912

Qy    222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241
          :::|||||||||   ||||||   |||||||||      :::|||            :::
Db    913 ATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTAC 972

Qy    242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly--------- 258
                :::::        |||        :::      :::|||
Db    973 TCATCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACA 1020

Qy    259 ---------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
                  |||      ||||||:::|||           ||||||::::::||||||
Db   1021 GCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTG 1080

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
          |||:::|||   :::||||||         |||      |||      :::
Db   1081 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG 1140

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
          ::::::   ||||||||||||:::::      ||||||:::   |||   |||||||||
Db   1141 CAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTCTGCTGG 1200

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
             ||||||:::||||||:::|||   |||   ||||||            :::
Db   1201 CTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG 1260

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
             |||   |||   :::   :::|||   |||         |||      ||||||
Db   1261 ACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATC 1320

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
          :::|||   ||||||||||||||:::|||||||||:::|||   |||||||||
Db   1321 CTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGA 1380

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          :::      :::|||         |||      ::::::      |||   :::
Db   1381 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC 1440

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
                |||         ||||||         ||||||
Db   1441 AGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1479

RESULT 15
HSIL8RB4
LOCUS       HSIL8RB4               2847 bp    DNA     linear   PRI 28-MAR-1995
DEFINITION  Human interleukin-8 receptor type B (IL8RB) gene, exons 10 and 11
            and complete cds.
ACCESSION   U11869
VERSION     U11869.1  GI:511801
KEYWORDS    .
SEGMENT     4 of 4
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2847)
  AUTHORS   Ahuja,S.K., Shetty,A., Tiffany,H.L. and Murphy,P.M.
  TITLE     Comparison of the genomic organization and promoter function for
            human interleukin-8 receptors A and B
  JOURNAL   J. Biol. Chem. 269 (42), 26381-26389 (1994)
  MEDLINE   95014476
REFERENCE   2  (bases 1 to 2847)
  AUTHORS   Ahuja,S.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-1994) Sunil K. Ahuja, Laboratory of Host
            Defenses, National Institutes of Health, National Institute of
            Allergy and Infectious Diseases, NIH, Bldg 10, Rm 11N109, Bethesda,
            MD 20892, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2q34-35"
                     /clone="9I"
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                     U11867.1:20. .71,1153. .2847)
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                     /note="alternatively spliced variant IL8RB1, exons 1,6,8
                     and 11"
     gene            join(U11866.1:1064. .2253,U11867.1:1. .88,U11868.1:1. .173,
                     1. .2847)
                     /gene="IL8RB"
     mRNA            join(U11866.1:1492. .1568,U11866.1:2077. .2139,
                     U11867.1:20. .71,1153. .2847)
                     /gene="IL8RB"
                     /note="alternatively spliced variant IL8RB2, exons 2,6,8
                     and 11"
     mRNA            join(U11866.1:1806. .1815,U11866.1:1856. .2139,
                     U11867.1:20. .71,1153. .2847)
                     /gene="IL8RB"
                     /note="alternatively spliced variant IL8RB3, exons 3,5,6,8
                     and 11"
     mRNA            join(U11866.1:1816. .1855,U11866.1:2077. .2139,
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                     and 11"
     mRNA            join(U11867.1:16. .71,1153. .2847)
                     /gene="IL8RB"
                     /note="alternatively spliced variant IL8RB7, exons 7,8 and
                     11"
     mRNA            join(U11868.1:16. .168,1153. .2847)
                     /gene="IL8RB"
                     /note="alternatively spliced variant IL8RB9, exons 9 and
                     11"
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                     /gene="IL8RB"
                     /number=5
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                     11"
     exon            972. .1152
                     /gene="IL8RB"
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BASE COUNT      727 a    758 c    629 g    733 t
ORIGIN

Alignment Scores:
Pred. No.:              2.57e-47        Length:         2847
Score:                  636.00          Matches:        150
Percent Similarity:     52.81%          Conservative:   57
Best Local Similarity:  38.27%          Mismatches:     139
Query Match:            29.57%          Indels:         46
DB:                     9               Gaps:           9

US-09-101-518A-2 (1-415) x HSIL8RB4 (1-2847)

Qy      43 ProSerSerProPhePro-----------------ProSerGlnValSerAspHisGln 56
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Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe---------------Ser 71
Db    1193 ATGGAGAGTGACAGC---------------TTTGAAGATTTCTGGAAAGGTGAAGATCTT 1237

Qy      72 SerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysPro 91
Db    1238 AGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGTGAA 1297

Qy      92 GlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPhe 111
Db    1298 CCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTATTC 1354

Qy     112 LeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAla 131
Db    1355 CTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTCGGC 1414

Qy     132 LeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeu 151
Db    1415 CGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCCCTG 1474

Qy     152 ThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCys 171
Db    1475 ACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTGTGC 1534

Qy     172 LysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCys 191
Db    1535 AAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCCTGC 1594

Qy     192 IleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyPro 211
Db    1595 ATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC------------------- 1636

Qy     212 ProAlaArgValThrLeuThr--------------------------CysLeuAlaVal 222
Db    1637 -----------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGCATC 1684

Qy     223 TrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAsp 242
Db    1685 TGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTACTCA 1744

Qy     243 GluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly------------ 258
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Db    1745 TCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACAGCA 1792

Qy     259 ------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
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Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db    1853 ATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGGCAG 1912

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
Db    1913 AAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTCTGCTGGCTG 1972

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
Db    1973 CCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAGACC 2032

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db    2033 TGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATCCTT 2092

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
Db    2093 CACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGACTC 2152

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
Db    2153 CTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGCAGG 2212

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSer 408
Db    2213 CCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 2248
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Job time : 2183 secs

GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:08:55 ; Search time 209 Seconds
(without alignments)
3409.184 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2142	99.6	1876	18	AAT72800	Human G-protein ch
2	2136	99.3	1877	22	AAH35033	Human colon cancer
3	1909	88.7	1159	20	AAZ32713	Human chemokine re
4	1897	88.2	1670	19	AAV26557	Human IP-10/Mig re
5	1891	87.9	1107	21	AAA30593	Human G protein-co
6	1885	87.6	1107	21	AAA30714	DNA encoding human
7	1627.5	75.7	1620	19	AAV43793	Rodent chemokine r
8	640.5	29.8	1068	24	ABK16598	DNA encoding verve
9	640	29.8	2517	20	AAX87709	Mouse Burkitt's ly
10	639.5	29.7	1068	24	ABK16599	DNA encoding baboo
11	637.5	29.6	1886	22	ABA09268	Human IL-8R B homo
12	637.5	29.6	2785	23	AAS77796	DNA encoding novel
13	636	29.6	12789	24	AAS16876	Human interleukin
14	635.5	29.5	1068	24	ABK16596	DNA encoding rhesu
15	635	29.5	1106	13	AAQ30012	Sequence encoding
16	635	29.5	1119	21	AAA30626	Human G protein-co
17	635	29.5	1510	14	AAQ38747	Human IL-8 recepto
18	635	29.5	1510	21	AAF20993	Human low adenosin
19	635	29.5	1510	21	AAA34871	Human adenosine re
20	635	29.5	1679	13	AAQ37107	New platelet facto
21	635	29.5	1679	16	AAQ99009	Chemokine superfam
22	635	29.5	1679	16	AAQ80522	Human lymphocyte P
23	635	29.5	1748	16	AAQ99008	Interleukin 8 rece
24	635	29.5	1750	21	AAF20991	Human low adenosin
25	635	29.5	1750	21	AAA34869	Human adenosine re
26	635	29.5	2818	20	AAX87710	Human Burkitt's ly
c 27	635	29.5	3620	22	ABA09117	Human Burkitt lymp
28	635	29.5	9319	21	AAF20995	Human low adenosin
29	635	29.5	9319	21	AAA34873	Human adenosine re
30	633	29.4	1068	17	AAA40128	Human IL-8 recepto
31	633	29.4	1068	24	ABK16589	DNA encoding human
32	633	29.4	1068	24	ABK16590	DNA encoding chima
33	633	29.4	1068	24	ABK16592	DNA encoding goril
34	633	29.4	1119	21	AAA30727	DNA encoding human
35	632.5	29.4	1068	24	ABK16594	DNA encoding orang
36	631.5	29.4	1068	24	ABK16597	DNA encoding rhesu
37	628	29.2	3011	24	AAS94899	Human DNA sequence
38	623	29.0	1068	24	ABK16595	DNA encoding orang
39	622.5	28.9	4017	23	AAS83768	DNA encoding novel
40	622	28.9	1053	24	ABK16591	DNA encoding chima
41	621.5	28.9	1200	13	AAQ30011	Sequence encoding
42	621.5	28.9	1200	16	AAQ99949	Recombinant high a
43	621	28.9	1068	24	ABK16593	DNA encoding goril
44	620	28.8	1106	16	AAQ99952	Recombinant high a
45	615	28.6	1373	16	AAQ99951	Recombinant high a

ALIGNMENTS

RESULT 1
AAT72800
ID AAT72800 standard; cDNA; 1876 BP.
XX
AC AAT72800;
XX
DT 28-SEP-1997 (first entry)
XX
DE Human G-protein chemokine receptor HSATU68 cDNA.
XX
KW HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;
KW signal transduction; gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 173..1420
FT /*tag= a

```
FT   primer_bind     complement (173..190)
FT                   /*tag=  b
FT   primer_bind     1402..1420
FT                   /*tag=  c
XX
PN   WO9725340-A1.
XX
PD   17-JUL-1997.
XX
PF   11-JAN-1996;   96WO-US00499.
XX
PR   11-JAN-1996;   96WO-US00499.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Li Y;
XX
DR   WPI; 1997-372810/34.
DR   P-PSDB; AAW19780.
XX
PT   DNA encoding new isolated human G-protein chemokine receptor - used
PT   to develop products for treating, e.g. autoimmune diseases, chronic
PT   infections, allergy, malignancy, inflammation or shock
XX
PS   Claim 1; Fig 1a-d; 54pp; English.
XX
CC   A cDNA clone (AAT72800) codes for a newly identified human G-protein
CC   chemokine receptor (AAW19780) designated HSATU68.  It was identified
CC   in a human genomic library derived from activated T cells.  HSATU68
CC   nucleic acids be used to produce HSATU68 in prokaryotic or
CC   eukaryotic host cells, as probes for the detection, screening and
CC   diagnosis of diseases caused by mutations in the HSATU68 gene, and
CC   in the gene therapy of conditions related to underexpression of the
CC   receptor its ligand.
XX
SQ   Sequence 1876 BP; 343 A; 625 C; 520 G; 388 T; 0 other;

Alignment Scores:
Pred. No.:              9.98e-230      Length:          1876
Score:                  2142.00        Matches:         414
Percent Similarity:     99.76%         Conservative:    0
Best Local Similarity:  99.76%         Mismatches:      1
Query Match:            99.58%         Indels:          0
DB:                     18             Gaps:            0

US-09-101-518A-2 (1-415) x AAT72800 (1-1876)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
           ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db     473 GCCTTCCTGCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy     121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy     141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 CACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy     161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy     181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy     201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy     221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy     241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGlnValGlyArgThr 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy     261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy     281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy     301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy     321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy     341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy     361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy     381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy     401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 2
AAH35033
ID   AAH35033 standard; cDNA; 1877 BP.
XX
AC   AAH35033;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human colon cancer antigen encoding cDNA SEQ ID NO:2115.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   colorectal carcinoma; chromosome 8; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75628.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3596-3597; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 1877 BP; 343 A; 625 C; 518 G; 388 T; 3 other;

Alignment Scores:

Pred. No.:	4.7e-229	Length:	1877
Score:	2136.00	Matches:	413
Percent Similarity:	99.52%	Conservative:	0
Best Local Similarity:	99.52%	Mismatches:	2
Query Match:	99.30%	Indels:	0
DB:	22	Gaps:	0

US-09-101-518A-2 (1-415) x AAH35033 (1-1877)

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Qy      1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
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Db    173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy     21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy     41 ThrAlaProSerSerProProheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
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Db    293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy     61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
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Db    353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy     81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
          |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 AGTGAMTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy    101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
          |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db    473 GCCTTCCTGCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy    121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
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Db    533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy    141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
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Db    593 CACCTAGCTGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy    161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy    181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy    201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy    221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
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Db    833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy    261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
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Db    953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy    281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
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Db   1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy    301 MetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
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Db   1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy    321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
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Db   1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
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Db   1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417
```

RESULT 3
AAZ32713
ID AAZ32713 standard; cDNA; 1159 BP.
XX
AC AAZ32713;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human chemokine receptor CXCR3b cDNA.

```
XX
KW   Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
KW   seven transmembrane; G-protein coupled; CXC; IP10; Mig; T-lymphocyte;
KW   recruitment; selective; activated; T-cell; neutrophil; inflammation;
KW   tissue distribution; therapy; rheumatoid arthritis; psoriasis;
KW   multiple sclerosis; transplantation; atherosclerosis; restenosis;
KW   cytokine; delayed type hypersensitivity reaction; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..52
FT                   /*tag= a
FT                   /note= "Novel exon found in CXCR3b transcripts"
FT   CDS             23..1159
FT                   /*tag= b
FT                   /product= "N-terminal fragment of CXCR3b"
XX
PN   WO9950299-A1.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-SE00501.
XX
PR   30-MAR-1998;   98SE-0001098.
XX
PA   (ASTR ) ASTRA PHARM LTD.
PA   (ASTR ) ASTRA AB.
XX
PI   Delaney S;
XX
DR   WPI; 1999-633638/54.
DR   P-PSDB; AAY50129.
XX
PT   New polynucleotide encoding a variant chemokine receptor -
XX
PS   Claim 1; Fig 2; 18pp; English.
XX
CC   This sequence represents cDNA encoding human chemokine receptor CXCR3b,
CC   a splice variant of chemokine receptor CXCR3 (also referred to as
CC   CXCR3a). Chemokines are a family of small cytokines which bring about the
CC   recruitment of leukocytes during inflammation. The CXC chemokines
CC   mostly attract neutrophils, while the CC chemokines are less selective.
CC   All chemokine receptors are seven transmembrane G-protein coupled
CC   receptors and most are receptors for a number of chemokines, CXCR3a
CC   being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is
CC   expressed in activated, but not in resting T-lymphocytes, and may
CC   therefore play an important role in the selective recruitment of
CC   T-cells which occurs in T-cell mediated inflammatory conditions.
CC   CXCR3b may have an altered pattern of tissue distribution and
CC   function in the inflammatory process. Cells expressing the active
CC   CXCR3b are useful for identifying ligands, especially agonists and
CC   antagonists, of a chemokine receptor. In addition, the receptor
CC   facilitates identification of chemokines responsible for mediating
CC   inflammation reactions via interaction with CXCR3b. The modulation
CC   of inflammatory responses is of therapeutic benefit in many conditions
CC   such as rheumatoid arthritis, psoriasis, multiple sclerosis,
CC   transplantation, delayed type hypersensitivity reactions, atherosclerosis
CC   and restenosis.
XX
SQ   Sequence 1159 BP; 177 A; 397 C; 343 G; 242 T; 0 other;

Alignment Scores:
Pred. No.:              6.33e-204      Length:          1159
Score:                  1909.00        Matches:         370
Percent Similarity:     97.89%         Conservative:    2
Best Local Similarity:  97.37%         Mismatches:      6
Query Match:            88.75%         Indels:          2
DB:                     20             Gaps:            1

US-09-101-518A-2 (1-415) x AAZ32713 (1-1159)

Qy      36 LeuProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55

           :::|||||||||      :::|||  |||      |||         ||||||||||||
Db      23 ATGCCAGGGCTGGCCCACAGCCCAGGGTCA------CCACAGGGTTGGGTGAGTGACCAC 76

Qy      56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAsp 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 136

Qy      76 TyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 196

Qy      96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 256

Qy     116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 316

Qy     136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 376

Qy     156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 436

Qy     176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 496

Qy     196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 556

Qy     216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 616

Qy     236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 676

Qy     256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     677 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTACCCCTG 736

Qy     276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     737 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 796

Qy     296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     797 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 856

Qy     316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     857 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 916

Qy     336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     917 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 976

Qy     356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     977 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1036

Qy     376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1037 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1096

Qy     396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db   1097 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1156

RESULT 4
AAV26557
ID   AAV26557 standard; DNA; 1670 BP.
XX
AC   AAV26557;
XX
DT   14-AUG-1998  (first entry)
XX
DE   Human IP-10/Mig receptor CXCR3 gene.
XX
KW   ds; chemokine receptor; cellular signal; treatment; T cell;
KW   inflammatory disease; antitumour; antiviral.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             69..1175
FT                   /*tag= a
FT                   /product= "IP-10/Mig receptor CXCR3"
FT   polyA_signal    1534..1539
FT                   /*tag= b
FT   polyA_site      1624..1670
FT                   /*tag= c
XX
PN   WO9811218-A1.
XX
PD   19-MAR-1998.
XX
PF   10-SEP-1997;   97WO-US15915.
XX
PR   31-MAR-1997;   97US-0829839.
PR   10-SEP-1996;   96US-0709838.
XX
PA   (KOCH-) KOCHER INST THEODOR.
PA   (LEUK-) LEUKOSITE INC.
XX
PI   Loetscher M,  Mackay CR,  Moser B,  Qin S;
XX
DR   WPI; 1998-207381/18.
DR   P-PSDB; AAW54371.
XX
PT   DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT   which, are useful for treatment of inflammation or in anti-tumour or
PT   anti-viral therapy
XX
PS   Claim 6; Fig 1; 137pp; English.
XX
CC   The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein
CC   which can selectively bind one or more chemokines and can mediate
CC   cellular signalling and/or a cellular response in response.  Inhibitors
CC   and promoters of mammalian CXCR3 can be detected and identified using
CC   host cells expressing CXCR3.  CXCR3 inhibitors can be used for treatment
CC   of inflammatory diseases which are T cell  mediated.  CXCR3 promoters are
CC   useful for antitumour or antiviral therapy.
XX
SQ   Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other;

Alignment Scores:
Pred. No.:              2.47e-202      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     19             Gaps:           1

US-09-101-518A-2 (1-415) x AAV26557 (1-1670)

Qy     41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
Db     36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
Db     96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
Db    156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
Db    216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
Db    276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
Db    336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
Db    396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
Db    456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
Db    516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
Db    576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
Db    636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
Db    696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
Db    756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
Db    816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy    317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
Db    876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy    337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
Db    936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy    357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
Db    996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy    377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
Db   1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy    397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
Db   1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 5
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```
AAA30593
ID   AAA30593 standard; cDNA; 1107 BP.
XX
AC   AAA30593;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human G protein-coupled receptor GPR9 cDNA.
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist; ss.
XX
OS   Homo sapiens.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   P-PSDB; AAY90614.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents  -
XX
PS   Example 1; Page 115; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. The present sequence represents cDNA encoding a human wild-type
CC   GPCR used in an exemplification of the invention. This was cloned and
CC   subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC   the corresponding mutant of the invention.
XX
SQ   Sequence 1107 BP; 163 A; 380 C; 324 G; 240 T; 0 other;

Alignment Scores:
Pred. No.:              6.15e-202      Length:         1107
Score:                  1891.00        Matches:        364
Percent Similarity:     100.00%        Conservative:   1
Best Local Similarity:  99.73%         Mismatches:     0
Query Match:            87.91%         Indels:         0
DB:                     21             Gaps:           0

US-09-101-518A-2 (1-415) x AAA30593 (1-1107)

Qy      51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy      71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy      91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy     111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy     131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy     151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy     171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy     191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 TGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGG 489

Qy     211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy     231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy     251 GlnTyrAsnProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy     271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729

Qy     291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy     311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy     331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     850 GGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACC 909

Qy     351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy     371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029

Qy     391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089
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Qy    411 SerTyrSerGlyLeu 415
          ||||||||||||||||
Db   1090 TCCTACTCGGGCTTG 1104
```

RESULT 6
AAA30714
ID AAA30714 standard; DNA; 1107 BP.
XX
AC AAA30714;
XX
DT 21-AUG-2000 (first entry)
XX
DE DNA encoding human mutant G protein-coupled receptor GPR9 (M254K).
XX
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
DR P-PSDB; AAY90648.
XX
PT Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
PS Example 2; Page 223; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 represent DNAs
CC encoding the mutant human GPCRs of the invention.
XX
SQ Sequence 1107 BP; 164 A; 380 C; 324 G; 239 T; 0 other;

Alignment Scores:

Pred. No.:	2.89e-201	Length:	1107
Score:	1885.00	Matches:	363
Percent Similarity:	99.73%	Conservative:	1
Best Local Similarity:	99.45%	Mismatches:	1

Query Match:	87.63%	Indels:	0
DB:	21	Gaps:	0

US-09-101-518A-2 (1-415) x AAA30714 (1-1107)

```
Qy      51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy      71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy      91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy     111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy     131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy     151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy     171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy     191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 TGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGG 489

Qy     211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy     231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy     251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy     271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729

Qy     291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
           |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db     730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCAAGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy     311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy     331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     850 GGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACC 909

Qy     351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy     371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029
```

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Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089

Qy    411 SerTyrSerGlyLeu 415
          |||||||||||||||
Db   1090 TCCTACTCGGGCTTG 1104

RESULT 7
AAV43793
ID   AAV43793 standard; cDNA; 1620 BP.
XX
AC   AAV43793;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Rodent chemokine receptor HST01.1 nucleotide sequence.
XX
KW   Chemokine; primate; human; rodent; chemokine receptor; asthma;
KW   inflammatory response; immune response; leukocyte migration; GPCR;
KW   leukocyte adhesion; chemoattractant; modulation; antiviral response;
KW   cellular morphology modification response; G-protein coupled receptor;
KW   phosphoinositide lipid turnover; abnormal proliferation; regeneration;
KW   atrophy; HST01.1; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1169
FT                   /*tag=  a
FT                   /product= "chemokine receptor HST01.1"
XX
PN   WO9832858-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US00902.
XX
PR   23-JAN-1997;   97US-0036715.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM,  Hedrick JA,  Mattson JD,  Soto-trejo H;
PI   Zlotnik A;
XX
DR   WPI; 1998-427954/36.
DR   P-PSDB; AAW69999.
XX
PT   Rodent and primate chemokines and chemokine receptors - useful
PT   diagnostically and therapeutically to treat conditions associated
PT   with abnormal physiology or development e.g. inflammatory conditions
XX
PS   Example 3; Pages 89-92; 105pp; English.
XX
CC   This represents a rodent chemokine receptor HST01.1 nucleotide sequence.
CC   The invention provides novel primate and rodent chemokines and chemokine
CC   receptors. The chemokines, receptors and binding compounds (optionally
CC   antibodies/fragments specifically binding the chemokines) are useful
CC   therapeutically to treat conditions associated with abnormal physiology
CC   or development e.g. inflammatory conditions such as asthma. Chemokines
CC   are important in immune and inflammatory responses in that they induce
CC   leukocyte migration and adhesion. They are also chemoattractants for
CC   several cells involved in inflammation and can induce other biological
CC   responses e.g. modulation of second messenger levels (e.g. Ca++),
CC   cellular morphology modification responses, phosphoinositide lipid
CC   turnover, possible antiviral responses etc. The chemokine receptors of
CC   the invention exhibit structural properties of G-protein coupled
CC   receptors (GPCR), although their ligands have not yet been identified.
CC   The chemokine and chemokine receptor polypeptides are useful to produce
CC   ligand:receptor complexes in vivo or in assay techniques. Assays may
CC   also involve chemical antagonists which block complex production or
CC   utilise competitive binding.  Binding compounds identified (agonists or
CC   antagonists) can be used to modulate the physiological responses in cells
CC   (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC   proliferation, regeneration, generation and atrophy. The polypeptides
CC   are also used to produce antibodies useful diagnostically, for drug
CC   screening or for polypeptide purification. The polynucleotides are useful
CC   to produce probes for detecting the polypeptides, and to isolate the
CC   polypeptides or related sequences, especially from other species. They
CC   also allow transformation of cells for polypeptide production.
XX
SQ   Sequence 1620 BP; 366 A; 457 C; 405 G; 392 T; 0 other;

Alignment Scores:
Pred. No.:              3.89e-172      Length:          1620
Score:                  1627.50        Matches:         316
Percent Similarity:     89.97%         Conservative:    25
Best Local Similarity:  83.38%         Mismatches:      37
Query Match:            75.66%         Indels:          1
DB:                     19             Gaps:            1

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Qy     37 ProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHisGln 56
          |||      ::::::      :::|||               :::|||||||:::   |||
Db     33 CCCAGCAGCCACAGCCGGAGCACCAGCCAAGCCATGTACCTTGAGGTTAGTGAACGTCAA 92

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
          ||||||:::   ::::::   |||  ||||||||||   :::|||   |||||||||
Db     93 GTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGCACCTCTCCCTACGATTAT 152

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
          ||||||||||||||||||           ||||||||||||||||||||||||||||||
Db    153 GGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGCCCACAGGATTTCAGCCTG 209

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
          ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db    210 AACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTCTTCTTGCTGGGGCTGCTA 269

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
          ||||||||||||||||||||||||||||||:::||||||||||||||||||||||||||
Db    270 GGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACTGCCCTGAGCAGCACGGAC 329

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    330 ACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTGTTAACTCTTCCATTGTGG 389

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    390 GCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCTGGCCTCTGCAAAGTGGCAGGCGCC 449

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
          ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    450 TTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTGCTGGCTTGTATAAGCTTCGACAGA 509

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
          ||||||:::|||||||||||||||||:::|||||||||   |||      ||||||
Db    510 TATCTGAGCATAGTGCACGCCACCCAGATCTACCGCAGGGACCCCCGGGTACGTGTAGCC 569

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
          |||||||||:::   ||||||||||||||||||||||||||||||||||||||||||:::
Db    570 CTCACCTGCATAGTTGTATGGGGTCTCTGTCTGCTCTTTGCCCTCCCAGATTTCATCTAC 629

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
          |||||||||::::::|||:::||||||||||||||||||||||||||||||||||||||
Db    630 CTATCAGCCAACTACGATCAGCGCCTCAATGCCACCCATTGCCAGTACAACTTCCCACAG 689

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 GTGGGTCGCACTGCTCTGCGTGTACTGCAGCTAGTGGCTGGTTTCCTGCTGCCCCTTCTG 749

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750 GTCATGGCCTACTGCTATGCCCATATCCTAGCTGTTCTGCTGGTCTCCAGAGGCCAGAGG 809

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
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              |||   ||||||||||||||||||||||||||||   ||||||||:::||||||||
Db     810 CGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTGGCAGCCTTTGCTGTCTGCTGGACC 869

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           |||||||||||||||||||||||||||||||||||||:::|||   |||||||||||
Db     870 CCCTATCACCTGGTGGTGCTAGTGGATATCCTCATGGATGTGGGAGTTTTGGCCCGCAAC 929

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           |||||||:::|||  |||||||||||||||||||||||||||||:::||||||||
Db     930 TGTGGTCGAAAAAGCCACGTGGATGTGGCCAAGTCAGTCACCTCGGGCATGGGGTACATG 989

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db     990 CACTGCTGCCTCAATCCGCTGCTCTATGCCTTTGTGGGAGTGAAGTTCAGAGAGAAAATG 1049

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||      ||||||||     :::|||||||||   |||||||||||||||
Db    1050 TGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAGAGAGGGCCCCAGCGGCAGCCGTCA 1109

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||:::|||||||||||||||||||:::||||||||||||    ||||||
Db    1110 TCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCTCCTACCTGGGCTTG 1166
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RESULT 8
ABK16598
ID   ABK16598 standard; DNA; 1068 BP.
XX
AC   ABK16598;
XX
DT   14-MAR-2002  (first entry)
XX
DE   DNA encoding vervet monkey CXCR2 receptor.
XX
KW   Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
KW   orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory;
KW   bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
XX
OS   Cercopithecus pygerythrus.
XX
PN   WO200190134-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16777.
XX
PR   22-MAY-2000; 2000US-0576160.
XX
PA   (PHAR-) PHARMACOPEIA INC.
XX
PI   Horlick R,  Zhao J,  Swanson R,  Webb M,  Strohl B,  Baldwin JJ;
PI   Auld DS;
XX
DR   WPI; 2002-106172/14.
DR   P-PSDB; AAU80491.
XX
PT   Identifying modulators of receptor activity using orthologues of human
PT   receptors by contacting a compound with receptors from two species, and
PT   measuring the effect of the compound on the receptors -
XX
PS   Claim 49; Page 100; 108pp; English.
XX
CC   The invention relates to identifying modulators of receptor activity
CC   using orthologues of human receptors by contacting a compound with
CC   receptors from two species, and measuring the effect of the compound on
CC   the receptors. Included is an isolated nucleic acid (I) comprising a
CC   nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a
CC   CXCR2 receptor (III). The method is useful for identifying a compound
CC   having dual specificity to modulate the activity of a desired polypeptide
CC   in two different species. The method is useful for identifying a non-
CC   human animal model for testing compounds with potential efficacy as human
CC   receptor modulators. The method comprises contacting a test compound with
CC   receptors from at least two species; measuring an effect of the compound
CC   on the receptors; and selecting an animal model representing a species
CC   having a receptor that exhibits the desired effect when contacted with
CC   the test compound. Also described is a method for identifying a compound
CC   that modulates (II) or (III) activity, where a compound is an agonist,
CC   antagonist, suppressor, inhibitor and inducer, useful in treatment of
CC   pain and inflammation and other receptor related pathologies. ABK16569-
CC   ABK16574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 receptor
CC   coding sequences of the invention.
XX
SQ   Sequence 1068 BP; 219 A; 325 C; 244 G; 280 T; 0 other;

Alignment Scores:
Pred. No.:                 9.54e-62      Length:          1068
Score:                     640.50        Matches:         145
Percent Similarity:        55.06%        Conservative:    51
Best Local Similarity:     40.73%        Mismatches:      129
Query Match:               29.78%        Indels:          31
DB:                        24            Gaps:            7

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```
Qy      68 GluAsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSer 87
           |||:::|||  |||:::|||  |||     :::        |||
Db      37 GAAGATTTT---AGTAATTACAGTTACAGCTCTGACCTGCCCCCTTCTCTACCAGATGTC 93

Qy      88 ProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyr 107
              ||||||    :::   ||||||    ::::::   |||:::      :::|||
Db      94 ACCCCATGTCGACCAGAA---TCCCTGGAAATCAACAAGTATTTGTGGTCATTATCTAT 150

Qy     108 SerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSer 127
           :::|||:::|||||||||   ||||||||||||       |||       |||:::|||
Db     151 GCCCTGGTATTCCTGCTGAGCTTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTACAC 210

Qy     128 ArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThr 147
              |||        |||   ||||||   :::||||||:::||||||:::||||||
Db     211 AGCAGGGTCGGCCGCTCCGTCACTGATGTCTACCTACTGAACCTGGCCATGGCCGACCTA 270

Qy     148 LeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGly 167
           |||     ||||||||||||:::||||||                   |||:::||||||
Db     271 CTGTTTGCCCTGACCTTGCCCATCTGGGCTGCCGCCAAGAAGAATGGCTGGATTTTTGGC 330

Qy     168 SerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeu 187
           :::   ||||||||||||          |||        :::|||||||||:::|||   |||
Db     331 ACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTACAGTGGCATCCTG 390

Qy     188 LeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyr 207
           ||||||||||||||||||   ||||||||||||   |||||||||||||||:::
Db     391 CTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC------ 444

Qy     208 ArgArgGlyProProAlaArgValThrLeuThr--------------------------- 218
                                    |||||||||
Db     445 -----------------------ACACTGACCCAGAAGCGCTACTTGGTCAAGTTCGTA 480

Qy     219 CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSer 238
           ||||||:::::|||||||||   ||||||   |||||||||         :::|||
Db     481 TGTCTCAGCATCTGGGGTCTGTCCTTACTCCTGGCCCTGCCCGTCTTACTTTTCCGAAGG 540

Qy     239 AlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly 258
              :::            ::::::       |||            :::      :::|||
Db     541 ACTGTCTACCCGACCTATATTAGCCCAGTC---TGC---------TATGAGGACATGGGC 588

Qy     259 ------------------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
                             |||      ||||||:::|||          ||||||:::
Db     589 AACAATACAGCAAAATGGCGGATGGTGTTGCGGATCCTGCCCCAGACCTTTGGCTTCATC 648

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSer 292
           ||||||||||||:::|||   :::||||||           |||      |||      :::
Db     649 TTGCCACTGCTGATCATGCTGTTCTGCTATGGATTCACCTTGCGCACGCTGTTTAAGGCC 708

Qy     293 ArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAla 312
                 ::::::   ||||||||||||::::::       ||||||:::    |||
Db     709 CACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTTGTCCTCATCTTCCTA 768

Qy     313 LeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAla 332
```

```
Db    769 CTCTGCTGGCTGCCCTACCACCTGGTCCTGCTGACAGACACTCTCATGAGGACCCGGTTG 828

Qy    333 LeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGly 352
Db    829 ATCAAGGAGACCTGTCAACGCCGCAATGACATCGACCGGGCCCTGGATGCCACCGAGATT 888

Qy    353 LeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPhe 372
Db    889 CTGGGCATCCTTCACAGCTGCCTCAACCCCATCATCTACGCCTTCATTGGCCAGAAGTTC 948

Qy    373 ArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGln 392
Db    949 CGCCATGGACTCCTCAAGATTCTAGCCACACATGGCTTGATCAGCAAGGACTCCCTGCCC 1008

Qy    393 ArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
Db   1009 AAAGACAGCAGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1056
```

RESULT 9
AAX87709
ID AAX87709 standard; cDNA; 2517 BP.
XX
AC AAX87709;
XX
DT 26-OCT-1999 (first entry)
XX
DE Mouse Burkitt's lymphoma receptor 1 (BLR1) cDNA.
XX
KW Burkitt's lymphoma receptor 1; BLR1; mouse;
KW B lymphocyte chemoattractant; BLC; chemokine; ligand;
KW drug screening; leukaemia; autoimmune disease; therapy; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..1125
FT /*tag= a
XX
PN WO9928468-A1.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US25561.
XX
PR 02-DEC-1997; 97US-0982493.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Cyster JG, Gunn MD, Williams LT;
XX
DR WPI; 1999-493764/41.
DR P-PSDB; AAY06643.
XX
PT Modulating interaction of a Burkitt's Lymphoma Receptor 1
PT polypeptide and ligand, useful in drug screens
XX
PS Example; Page 33-34; 42pp; English.
XX
CC This is the nucleotide sequence of murine cDNA coding for a
CC Burkitt's lymphoma receptor 1 (BLR1, see AAY06643). The invention
CC relates to methods for modulating the interaction of BLR1 with
CC its ligand, B lymphocyte chemoattractant (BLC, see AAY06641). The
CC methods comprise combining BLR1 and BLC polypeptides with a
CC candidate modulator agent under conditions whereby, but for the
CC presence of the agent, the polypeptides engage in a first
CC interation, and determining a second interaction of the
CC polypeptides in the presence of the agent, wherein a difference
CC between the first and second interactions indicates that the agent
CC modulates the interaction of the polypeptides. The modulator is
CC preferably an antagonist, especially dominant negative, form of
CC BLC. BLC and BLC agonists and antagonists may be useful for
CC treating viral (e.g. HIV) infections, lymphoma, B lineage
CC leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC thyroiditis and diabetes.
XX
SQ Sequence 2517 BP; 620 A; 727 C; 601 G; 569 T; 0 other;

Alignment Scores:

Pred. No.:	4.09e-61	Length:	2517
Score:	640.00	Matches:	143
Percent Similarity:	56.29%	Conservative:	54
Best Local Similarity:	40.86%	Mismatches:	139
Query Match:	29.75%	Indels:	14
DB:	20	Gaps:	6

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Qy     70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
Db     76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy     90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
Db    127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186

Qy    110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
Db    187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy    130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
Db    247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy    150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
Db    307 GTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy    170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
Db    367 CTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTCGTG 426

Qy    190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
Db    427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy    210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
Db    487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy    230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
Db    547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

Qy    247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr------------AlaLeu 262
Db    604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
Db    661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
Db    721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy    302 ArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
Db    781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840

Qy    322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
Db    841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy    342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
```

```
Db    901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy    362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
          |||:::||||||   |||   ||||||||||||||      :::      ||||||
Db    961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy    382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
          :::||||||||||              |||      |||         :::   |||
Db   1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy    402 SerSerTrpSerGluThrSerGluAlaSer 411
          ||||||   ||||||:::      |||:::
Db   1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107

RESULT 10
ABK16599
ID   ABK16599 standard; DNA; 1068 BP.
XX
AC   ABK16599;
XX
DT   14-MAR-2002  (first entry)
XX
DE   DNA encoding baboon CXCR2 receptor.
XX
KW   Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
KW   orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory;
KW   bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
XX
OS   Papio hamadryus.
XX
PN   WO200190134-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16777.
XX
PR   22-MAY-2000; 2000US-0576160.
XX
PA   (PHAR-) PHARMACOPEIA INC.
XX
PI   Horlick R,  Zhao J,  Swanson R,  Webb M,  Strohl B,  Baldwin JJ;
PI   Auld DS;
XX
DR   WPI; 2002-106172/14.
DR   P-PSDB; AAU80492.
XX
PT   Identifying modulators of receptor activity using orthologues of human
PT   receptors by contacting a compound with receptors from two species, and
PT   measuring the effect of the compound on the receptors -
XX
PS   Claim 49; Page 100-101; 108pp; English.
XX
CC   The invention relates to identifying modulators of receptor activity
CC   using orthologues of human receptors by contacting a compound with
CC   receptors from two species, and measuring the effect of the compound on
CC   the receptors. Included is an isolated nucleic acid (I) comprising a
CC   nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a
CC   CXCR2 receptor (III). The method is useful for identifying a compound
CC   having dual specificity to modulate the activity of a desired polypeptide
CC   in two different species. The method is useful for identifying a non-
CC   human animal model for testing compounds with potential efficacy as human
CC   receptor modulators. The method comprises contacting a test compound with
CC   receptors from at least two species; measuring an effect of the compound
CC   on the receptors; and selecting an animal model representing a species
CC   having a receptor that exhibits the desired effect when contacted with
CC   the test compound. Also described is a method for identifying a compound
CC   that modulates (II) or (III) activity, where a compound is an agonist,
CC   antagonist, suppressor, inhibitor and inducer, useful in treatment of
CC   pain and inflammation and other receptor related pathologies. ABK16569-
CC   ABK16574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 receptor
CC   coding sequences of the invention.
XX
SQ   Sequence 1068 BP; 214 A; 327 C; 244 G; 282 T; 1 other;

Alignment Scores:
Pred. No.:              1.24e-61        Length:         1068
Score:                  639.50          Matches:        145
Percent Similarity:     56.45%          Conservative:   52
Best Local Similarity:  41.55%          Mismatches:     135
Query Match:            29.73%          Indels:         17
DB:                     24              Gaps:           7

US-09-101-518A-2 (1-415) x ABK16599 (1-1068)

Qy     68 GluAsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSer 87
          |||:::|||   |||:::|||   |||      :::         |||
Db     37 GAAGATTTT---AGTAATTACAGTTACAGCTCTGACCTGCCCCCTTCTCTACCAGATGTC 93

Qy     88 ProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyr 107
          ||||||      :::   ||||||      ::::::   |||:::      :::|||
Db     94 GCCCCATGTCGACCAGAA---TCCCTAGAAATCAACAAGTATTTTGTGGTCATTATCTAT 150

Qy    108 SerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSer 127
          :::|||:::|||||||||   ||||||||||||      |||      |||:::|||
Db    151 GCCCTGGTATTCCTGCTGAGCTTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTACAC 210

Qy    128 ArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThr 147
          |||         |||   ||||||   :::|||||||:::||||||:::||||||
Db    211 AGCAGGGTCGGCCGCTCCATCACTGATGTCTACCTACTGAACCTGGCCATGGCCGACCTA 270

Qy    148 LeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGly 167
          |||      ||||||||||||:::||||||                  |||:::|||||
Db    271 CTGTTTGCCCTGACCTTGCCCATCTGGGCTGCCGCCAAGGTGAATGGCTGGATTTTTGGC 330

Qy    168 SerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeu 187
          :::   ||||||||||||         |||      :::|||||||||:::|||   |||
Db    331 ACATTCCTGTGCAAAGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTG 390

Qy    188 LeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGln------ 205
          ||||||||||||||||||   ||||||||||||   ||||||||||||||||:::
Db    391 CTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGCACACTG 450

Qy    206 LeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeu 225
          :::   :::|||                  |||         ||||||::::::||||||||||
Db    451 ATCCAGAAGCGC---------TACTTGGTCAAGTTCATATGCCTCAGCATCTGGGGTCTG 501

Qy    226 CysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeu 245
          ||||||   |||||||||      :::|||      |||   :::         :::
Db    502 TCCTTGCTCCTGGCCCTGCCCGTCTTACTTTTCCGAAGGGCTGTCTACCCRCCCTATATT 561

Qy    246 AsnAlaThrHisCysGlnTyrAsnProProGlnValGly------------------Arg 259
          :::         |||         :::      :::|||                    |||
Db    562 AGCCCAGTC---TGC---------TATGAGGACATGGGCAACAATACAGCAAAATGGCGG 609

Qy    260 ThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAla 279
                ||||||:::|||            ||||||::::::||||||||||:::|||
Db    610 ATGGTGTTGCGGATCCTGCCCCAGACCTTTGGCTTCATCGTGCCGCTGCTGATCATGCTG 669

Qy    280 TyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArg 299
          :::||||||         |||      |||      :::      ::::::   |||
Db    670 TTCTGCTATGGATTCACCCTGCGCACGCTGTTTAAGGCCCACATGGGGCAGAAGCACCGG 729

Qy    300 AlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHis 319
          |||||||||::::::      ||||||:::   |||   |||||||||   |||||||||
Db    730 GCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTACTTTGCTGGCTGCCCTACCAC 789

Qy    320 LeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArg 339
          ||||||:::|||   |||   ||||||            :::         |||   |||
Db    790 CTGGTCCTGCTGGCAGACACCCTCATGAGGACCCGGTTGATCAACGAGACCTGTCAGCGC 849

Qy    340 GluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCys 359
          |||   ::::::   |||      |||      ||||||      |||   |||
Db    850 CACAGTGACATCAACCAGGCCCTGGATGCCACCGAGATTCTGGGCATCTTTCACAGCTGC 909

Qy    360 LeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeu 379
          ||||||||||||:::|||||||||:::|||   |||||||||      :::      :::
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```
Db    910 CTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTCCGCCATGGACTCCTCAAGATT 969

Qy    380 LeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArg 399
          |||        |||      ::::::     |||   :::            |||
Db    970 CTAGCCACACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGCAGGCCTTCCTTT 1029

Qy    400 ArgAspSerSerTrpSerGluThrSer 408
              ||||||        ||||||
Db   1030 GTTGGCTCTTCTTCAGGACACACTTCC 1056

RESULT 11
ABA09268
ID   ABA09268 standard; cDNA; 1886 BP.
XX
AC   ABA09268;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human IL-8R B homologue-encoding cDNA, SEQ ID NO:1044.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US03800.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   P-PSDB; ABB12024.
XX
PT   Human proteins and DNA encoding sequences useful for preventing,
PT   treating or ameliorating a medical condition in a mammalian subject
PT   e.g. arthritis and cancer -
XX
PS   Claim 1; Page 874; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention.
XX
SQ   Sequence 1886 BP; 428 A; 556 C; 418 G; 484 T; 0 other;

Alignment Scores:
Pred. No.:              4.99e-61      Length:          1886
Score:                  637.50        Matches:         154
Percent Similarity:     51.09%        Conservative:    57
Best Local Similarity:  37.29%        Mismatches:      145
Query Match:            29.64%        Indels:          57
DB:                     22            Gaps:            10

US-09-101-518A-2 (1-415) x ABA09268 (1-1886)

Qy     17 GlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeu 36
          ||||||      |||   ||||||
Db    349 GGAGGTGTCCTACAGGTGAAAAGC---------------------------------- 372

Qy     37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55
                       |||      |||   |||         |||::::::   |||
Db    373 ------------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT 420

Qy     56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe--------------- 70
             :::   :::|||:::                  |||:::|||   .
Db    421 AACATGGAGAGTGACAGC--------------TTTGAAGATTTCTGGAAAGGTGAAGAT 465

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
          |||:::|||   |||                                  :::   ||||||
Db    466 CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT 525

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
             :::   ||||||      ::::::   |||:::      :::|||:::|||:::
Db    526 GAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA 582

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
          |||||||||   ||||||||||||      |||      |||:::|||      |||
Db    583 TTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTC 642

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
             |||   ||||||   :::||||||:::||||||:::||||||   |||
Db    643 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC 702

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||||||||:::||||||                  |||:::||||||:::   |||
Db    703 CTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTG 762

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          |||||||||         |||      :::|||||||||:::|||   ||||||||||||
Db    763 TGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCC 822

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
          |||||||||   ||||||||||||   ||||||||||||||:::
```

```
Db     823 TGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC-------------- 867

Qy     211 ProProAlaArgValThrLeuThr--------------------------CysLeuAla 221
                          |||||||||                           ||||||:::
Db     868 ---------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGC 912

Qy     222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241
            :::|||||||||   ||||||   |||||||||       :::|||             :::
Db     913 ATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTAC 972

Qy     242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly--------- 258
                    ::::::      |||       :::      :::|||
Db     973 TCATCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACA 1020

Qy     259 ---------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
                     |||       ||||||:::|||           ||||||::::::||||||
Db    1021 GCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTG 1080

Qy     276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
            |||:::|||   :::||||||           |||      |||       :::
Db    1081 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG 1140

Qy     296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
            ::::::   ||||||||||||::::::          |||||||:::   |||   |||||||||
Db    1141 CAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTTTGCTGG 1200

Qy     316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
               ||||||:::||||||:::|||   |||   ||||||             :::
Db    1201 CTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG 1260

Qy     336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
               |||   |||   :::    :::|||   |||        |||     ||||||
Db    1261 ACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATC 1320

Qy     356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
            :::|||   |||||||||||||||:::||||||||||:::|||    |||||||||
Db    1321 CTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGA 1380

Qy     376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
            :::      :::|||         |||      ::::::      |||   :::
Db    1381 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC 1440

Qy     396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
                 |||          ||||||          ||||||
Db    1441 AGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1479
```

RESULT 12
AAS77796

```
ID   AAS77796 standard; cDNA; 2785 BP.
XX
AC   AAS77796;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #13600.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG13609.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 13600; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2785 BP; 739 A; 722 C; 629 G; 695 T; 0 other;
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Alignment Scores:

Pred. No.:	9.11e-61	Length:	2785
Score:	637.50	Matches:	154
Percent Similarity:	51.09%	Conservative:	57
Best Local Similarity:	37.29%	Mismatches:	145
Query Match:	29.64%	Indels:	57
DB:	23	Gaps:	10

US-09-101-518A-2 (1-415) x AAS77796 (1-2785)

```
Qy      17 GlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeu 36
            ||||||        |||   ||||||
Db     349 GGAGGTGTCCTACAGGTGAAAAGC------------------------------------ 372

Qy      37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55
                             |||      |||   |||         |||::::::   |||
Db     373 ------------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT 420

Qy      56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe--------------- 70
              :::   :::|||:::                    |||:::|||
Db     421 AACATGGAGAGTGACAGC---------------TTTGAAGATTTCTGGAAAGGTGAAGAT 465

Qy      71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
              |||:::|||   |||                                 :::   ||||||
Db     466 CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT 525

Qy      91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
                 :::   ||||||      ::::::   |||:::       :::|||:::|||:::
Db     526 GAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA 582

Qy     111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
            |||||||||   ||||||||||||         |||         |||:::|||      |||
Db     583 TTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTC 642

Qy     131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
               |||   ||||||      :::||||||:::||||||:::||||||      |||
Db     643 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC 702
```

```
Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
Db    703 CTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTG 762

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
Db    763 TGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCC 822

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
Db    823 TGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC---------------- 867

Qy    211 ProProAlaArgValThrLeuThr----------------------------CysLeuAla 221
Db    868 --------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGC 912

Qy    222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241
Db    913 ATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTAC 972

Qy    242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly--------- 258
Db    973 TCATCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACA 1020

Qy    259 ---------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
Db   1021 GCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTG 1080

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
Db   1081 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG 1140

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
Db   1141 CAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTCTGCTGG 1200

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
Db   1201 CTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG 1260

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
Db   1261 ACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATC 1320

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
Db   1321 CTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGA 1380

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
Db   1381 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC 1440

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
Db   1441 AGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1479
```

RESULT 13
AAS16876
ID AAS16876 standard; DNA; 12789 BP.
XX
AC AAS16876;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human interleukin 8 receptor beta (IL8RB) genomic DNA.
XX
KW Human; interleukin 8 receptor beta; IL8RB; ds; antiinflammatory;
KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;
KW gene therapy; drug screening; chronic obstructive pulmonary disease;
KW inflammatory disease.
XX
OS Homo sapiens.
XX

FH Key   Location/Qualifiers
FT CDS   9572..10654
FT   /*tag= a
FT   /product= "Human IL8RB"
FT   /note= "This coding sequence is specifically claimed in
FT   the specification"
FT variation   replace(1082,A)
FT   /*tag= b
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10277,T)
FT   /*tag= c
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10292,A)
FT   /*tag= d
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10327,T)
FT   /*tag= e
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10339,T)
FT   /*tag= f
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10507,T)
FT   /*tag= g
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10612,T)
FT   /*tag= h
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10780,C)
FT   /*tag= i
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10925,C)
FT   /*tag= j
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(10991,G)
FT   /*tag= k
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(11008,T)
FT   /*tag= l
FT   /standard_name= "Single nucleotide polymorphism"
FT variation   replace(11012,A)
FT   /*tag= m
FT   /standard_name= "Single nucleotide polymorphism"
XX
PN WO200179221-A2.
XX
PD 25-OCT-2001.
XX
PF 12-APR-2001; 2001WO-US11942.
XX
PR 12-APR-2000; 2000US-196734P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bentivegna SC, Chew A, Choi JY, Denton RR, Nandabalan K;
XX
DR WPI; 2002-055250/07.
DR P-PSDB; AAU10557.
XX
PT New polymorphic variants comprising interleukin-8 receptor beta (IL8RB)
PT isogene, useful in expressing IL8RB protein for use in screening for
PT candidate drugs to treat diseases related to IL8RB activity, e.g.
PT inflammatory disorders -
XX
PS Claim 21; Fig 1; 74pp; English.
XX
CC The invention relates to single nucleotide polymorphisms in the human
CC interleukin 8 receptor beta (IL8RB) gene. A method for haplotyping the
CC IL8RB gene in an individual comprises identifying the nucleotide at one
CC or more polymorphic sites and determining whether one of the copies of
CC the gene is defined by one of the IL8RB haplotypes given in the
CC specification or whether both copies are defined by a haplotype pair.
CC This method is useful in genotyping, whereby all possible haplotype pairs
CC can be assigned to specific genotypes. An association between a trait and
```
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CC   a haplotype or haplotype pair of the IL8RB gene can be identified by
CC   comparing the frequency of the haplotype or haplotype pair in a
CC   population exhibiting the trait with the frequency of the haplotype or
CC   haplotype pair in a reference population, where a higher haplotype
CC   frequency in the trait population indicates the trait is associated with
CC   the haplotype or haplotype pair. IL8RB and its corresponding DNA are used
CC   for studying the expression and function of IL8RB, for use in screening
CC   for candidate drugs to treat diseases related to IL8RB activity, such as
CC   chronic obstructive pulmonary disease and other inflammatory disorders.
CC   The sequences are also useful for studying the effect of variation on the
CC   biological activity of IL8RB as well as on the binding affinity of
CC   candidate drugs targeting IL8RB. This sequence represents genomic DNA
CC   encoding IL8RB.
XX
SQ   Sequence 12789 BP; 3363 A; 3042 C; 2867 G; 3510 T; 7 other;

Alignment Scores:
Pred. No.:                1.42e-59       Length:          12789
Score:                    636.00         Matches:         150
Percent Similarity:       52.81%         Conservative:    57
Best Local Similarity:    38.27%         Mismatches:      139
Query Match:              29.57%         Indels:          46
DB:                       24             Gaps:            9

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Qy      43 ProSerSerProPhePro----------------ProSerGlnValSerAspHisGln 56
           |||||||||   |||                   |||::::::   |||
Db    9527 CCTTCATCTCTCTTCTATAGGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTTAAC 9586

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe--------------Ser 71
           :::   :::|||:::                  |||:::|||
Db    9587 ATGGAGAGTGACAGC--------------TTTGAAGATTTCTGGAAAGGTGAAGATCTT 9631

Qy      72 SerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysPro 91
           |||:::|||   |||                        :::   ||||||
Db    9632 AGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGTGAA 9691

Qy      92 GlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPhe 111
             :::   ||||||      ::::::   |||:::      :::|||:::|||:::|||
Db    9692 CCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTATTC 9748

Qy     112 LeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAla 131
           ||||||   ||||||||||||      |||      |||:::|||      |||
Db    9749 CTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTCGGC 9808

Qy     132 LeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeu 151
             |||   ||||||   :::||||||:::||||||:::||||||   |||      |||
Db    9809 CGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCCCTG 9868

Qy     152 ThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCys 171
           |||||||||:::||||||                  |||:::||||||:::   ||||||
Db    9869 ACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTGTGC 9928

Qy     172 LysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCys 191
           ||||||         |||      :::||||||||||:::|||   ||||||||||||||
Db    9929 AAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCCTGC 9988

Qy     192 IleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyPro 211
           ||||||   ||||||||||||   ||||||||||||||:::
Db    9989 ATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC---------------------- 10030

Qy     212 ProAlaArgValThrLeuThr--------------------------CysLeuAlaVal 222
                   |||||||||                              ||||||::::::
Db   10031 ------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGCATC 10078

Qy     223 TrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAsp 242
           |||||||||   ||||||   |||||||||      :::|||            :::
Db   10079 TGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTACTCA 10138

Qy     243 GluArgLeuAsnAlaThrHisCysGlnTyrAsnProGlnValGly------------ 258
             ::::::      |||       :::      :::|||
Db   10139 TCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACAGCA 10186

Qy     259 ------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
                  |||      ||||||:::|||            ||||||::::::|||||||||
Db   10187 AACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTGCTG 10246

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           :::|||   :::||||||         |||      |||      :::        :::
Db   10247 ATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGGCAG 10306

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
           :::   ||||||||||||::::::      ||||||:::   |||   |||||||||
Db   10307 AAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTCTGCTGGCTG 10366

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||:::||||||:::|||   |||   ||||||              :::
Db   10367 CCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAGACC 10426

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           |||   |||   :::   :::|||   |||         |||      ||||||   :::
Db   10427 TGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATCCTT 10486

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           |||   ||||||||||||||:::|||||||||:::|||   |||||||||      :::
Db   10487 CACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGACTC 10546

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
                 :::|||         |||      ::::::      |||   :::
Db   10547 CTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGCAGG 10606

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSer 408
              |||         ||||||         ||||||
Db   10607 CCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 10642

RESULT 14
ABK16596
ID   ABK16596 standard; DNA; 1068 BP.
XX
AC   ABK16596;
XX
DT   14-MAR-2002  (first entry)
XX
DE   DNA encoding rhesus macaque CXCR2 receptor #1.
XX
KW   Human; baboon; chimpanzee; vervet monkey; rhesus macaque;
KW   orangutan; gorilla; tree shrew; dog; analgesic; antiinflammatory;
KW   bradykinin 1 receptor; CXCR2 receptor; pain; inflammation; ds.
XX
OS   Macaca mulatta.
XX
PN   WO200190134-A1.
XX
PD   29-NOV-2001.
XX
PF   22-MAY-2001; 2001WO-US16777.
XX
PR   22-MAY-2000; 2000US-0576160.
XX
PA   (PHAR-) PHARMACOPEIA INC.
XX
PI   Horlick R,  Zhao J,  Swanson R,  Webb M,  Strohl B,  Baldwin JJ;
PI   Auld DS;
XX
DR   WPI; 2002-106172/14.
DR   P-PSDB; AAU80489.
XX
PT   Identifying modulators of receptor activity using orthologues of human
PT   receptors by contacting a compound with receptors from two species, and
PT   measuring the effect of the compound on the receptors -
XX
PS   Claim 49; Page 98-99; 108pp; English.
XX
CC   The invention relates to identifying modulators of receptor activity
CC   using orthologues of human receptors by contacting a compound with
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CC   receptors from two species, and measuring the effect of the compound on
CC   the receptors. Included is an isolated nucleic acid (I) comprising a
CC   nucleotide sequence encoding bradykinin B1 receptor (II); or encoding a
CC   CXCR2 receptor (III). The method is useful for identifying a compound
CC   having dual specificity to modulate the activity of a desired polypeptide
CC   in two different species. The method is useful for identifying a non-
CC   human animal model for testing compounds with potential efficacy as human
CC   receptor modulators. The method comprises contacting a test compound with
CC   receptors from at least two species; measuring an effect of the compound
CC   on the receptors; and selecting an animal model representing a species
CC   having a receptor that exhibits the desired effect when contacted with
CC   the test compound. Also described is a method for identifying a compound
CC   that modulates (II) or (III) activity, where a compound is an agonist,
CC   antagonist, suppressor, inhibitor and inducer, useful in treatment of
CC   pain and inflammation and other receptor related pathologies. ABK16569-
CC   ABK16574 and ABK16589-ABK16599 represent bradykinin 1 and CXCR2 receptor
CC   coding sequences of the invention.
XX
SQ   Sequence 1068 BP; 216 A; 324 C; 245 G; 283 T; 0 other;

Alignment Scores:
Pred. No.:              3.47e-61      Length:          1068
Score:                  635.50        Matches:         146
Percent Similarity:     53.61%        Conservative:    47
Best Local Similarity:  40.56%        Mismatches:      128
Query Match:            29.54%        Indels:          39
DB:                     24            Gaps:            7

US-09-101-518A-2 (1-415) x ABK16596 (1-1068)

Qy      68 GluAsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSer 87
           |||:::|||   |||:::|||  |||      :::        |||
Db      37 GAAGATTTT---AGTAATTACAGTTACAGCTCTGACCTGCCCCCTTCTCTACCAGATGTC 93

Qy      88 ProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyr 107
             ||||||      :::   ||||||      ::::::   |||:::      :::|||
Db      94 GCCCCATGTCGACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTAT 150

Qy     108 SerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSer 127
           :::|||:::|||||||||   ||||||||||      |||      |||:::|||
Db     151 GCCCTGGTATTCCTGCTGAGCTTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTACAC 210

Qy     128 ArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThr 147
             |||         |||   ||||||   :::||||||:::||||||:::||||||
Db     211 AGCAGGGTCGGCCGCTCCATCACTGATGTCTACCTACTGAACCTGGCCATGGCCGACCTA 270

Qy     148 LeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGly 167
           |||      ||||||||||||:::||||||                  |||:::||||||
Db     271 CTGTTTGCCCTGACCTTGCCCATCTGGGCTGCCGCCAAGGTGAATGGCTGGATTTTTGGC 330

Qy     168 SerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeu 187
           :::   ||||||||||||         |||      :::||||||||:::|||   |||
Db     331 ACATTCCTGTGCAAAGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTG 390

Qy     188 LeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyr 207
           ||||||||||||||||   ||||||||||||  ||||||||||||||:::
Db     391 CTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC------ 444

Qy     208 ArgArgGlyProProAlaArgValThrLeuThr-------------------------- 218
                           |||||||||
Db     445 ----------------------ACACTGACCCAGAAGCGCTACTTGGTCAAGTTCGTA 480

Qy     219 CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSer 238
           ||||||::::::|||   |||   ||||||   |||||||||      :::|||
Db     481 TGTCTCAGCATCTGGAGTCTATCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTC------ 534

Qy     239 AlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro--------- 255
                                       :::      |||      |||
Db     535 -----------------CGAAGGACTGTCTACCTGACCTATATTAGCCCAGTCTGCTAT 576

Qy     256 ---GlnValGly-----------------ArgThrAlaLeuArgValLeuGlnLeuVal 268
              :::|||                  |||      ||||||:::|||
Db     577 GAGGACATGGGCAACAATACAGCAAAATGGCGGATGGTGTTGCGGATCCTGCCCCAGACC 636

Qy     269 AlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaVal 288
           ||||||:::|||||||||||||:::|||   :::||||||         |||
Db     637 TTTGGCTTCATCTTGCCGCTGCTGATCATGCTGTTCTGCTATGGATTGACCCTGCGCACG 696

Qy     289 LeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValVal 308
           |||      :::         ::::::   ||||||||||||::::::      ||||||
Db     697 CTGTTTAAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTC 756

Qy     309 ValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMet 328
           :::   |||   |||||||||   |||||||||||||||:::|||   |||   ||||||
Db     757 CTCATCTTCCTACTCTGCTGGCTGCCTTACCACCTGGTCCTGCTGGCAGACACCCTCATG 816

Qy     329 AspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSer 348
                   :::         |||   |||   :::   :::|||   |||
Db     817 AGGACCCGGTTGATCAACGAGACCTGTCAGCGCCGCAACAACATCGACCAGGCCCTGGAT 876

Qy     349 ValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheVal 368
           |||      ||||||   :::|||   |||||||||||||||:::||||||||||:::
Db     877 GCCACCGAGATTCTGGGCATCCTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATT 936

Qy     369 GlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGln 388
           |||   |||||||||      :::      :::|||          |||      ::::::
Db     937 GGCCAGAAGTTTCGCCATGGACTCCTCAAGATTCTAGCCACACATGGCTTGATCAGCAAG 996

Qy     389 ArgGlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
                 |||   :::             |||         ||||||         ||||||
Db     997 GACTCCCTGCCCAAAGACAGCAGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1056

RESULT 15
AAQ30012
ID   AAQ30012 standard; cDNA; 1106 BP.
XX
AC   AAQ30012;
XX
DT   04-APR-1993  (first entry)
XX
DE   Sequence encoding a low affinity recombinant human interleukin-8
DE   (IL-8) receptor polypeptide in 4AB.
XX
KW   IL-8 receptor polypeptide; G-protein-coupled receptor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             13..1095
FT                   /*tag=  a
XX
PN   WO9218641-A.
XX
PD   29-OCT-1992.
XX
PF   10-APR-1992;   92WO-US02977.
XX
PR   10-APR-1991;   91US-0685101.
PR   09-JUL-1991;   91US-0726606.
PR   09-DEC-1991;   91US-0803842.
XX
PA   (REPK ) REPLIGEN CORP.
PA   (UYBO-) UNIV BOSTON.
XX
PI   Navarro J,  Thomas KM,  Witt DP;
XX
DR   WPI; 1992-382123/46.
DR   P-PSDB; AAR28273.
XX
PT   Recombinant mammalian interleukin-8 receptor - used for screening
PT   interleukin-8 binding antagonists, used to treat inflammation
XX
PS   Disclosure; Fig 2; 71pp; English.
XX
CC   Rabbit high affinity IL-8 receptor gene was isolated from rabbit
CC   peritoneal neutrophils and used as a source of poly(A)+ RNA, to
```

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CC   produce a rabbit neutrophil cDNA library.  250,000 recombinant
CC   plaques were screened for those which hybridized to an antisense
CC   oligonucleotide (AAQ30015).  This probe was designed based on the
CC   sequence derived from the second transmembrane domain of G-protein-
CC   coupled receptors.  After tertiary screening, six plaques were
CC   isolated.  The insert of one of these plaques, termed F3R was of 2.5
CC   kb in size.  This insert was sequenced.  The protein deduced from
CC   the F3R clone demonstrates that it belongs to the family of
CC   G-protein-coupled receptors.  The deduced protein sequence
CC   indicates seven putatuve transmembrane segments.  A human
CC   peripheral blood leukocyte lambda gt11 cDNA library (5' stretch) was
CC   screened with a 652 bp EcoRI/BamHI fragment (including nucleotides
CC   -27 to 625) of the rabbit F3R clone.  After tertiary screening
CC   several human clones which hybridized to the rabbit IL-8 probe
CC   were isolated.  The insert of one such clone, termed 4AB was
CC   sequenced (AAQ30012).
XX
SQ   Sequence 1106 BP; 225 A; 336 C; 251 G; 294 T; 0 other;

Alignment Scores:
Pred. No.:                4.17e-61      Length:          1106
Score:                    635.00        Matches:         146
Percent Similarity:       53.56%        Conservative:    57
Best Local Similarity:    38.52%        Mismatches:      136
Query Match:              29.52%        Indels:          40
DB:                       13            Gaps:            8

US-09-101-518A-2 (1-415) x AAQ30012 (1-1106)

Qy      50 SerGlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsn 69
           |||::::::   |||      :::   :::|||:::                 |||:::
Db       7 TCAAAAATGGAAGATTTTAACATGGAGAGTGACAGC---------------TTTGAAGAT 51

Qy      70 Phe--------------SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCys 84
           |||               |||:::|||   |||
Db      52 TTCTGGAAAGGTGAAGATCTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTA 111

Qy      85 CysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuPro 104
               :::   ||||||      :::   ||||||      ::::::   |||:::
Db     112 CTAGATGCCGCCCCATGTGAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTC 168

Qy     105 AlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaVal 124
           :::|||:::|||:::|||||||||   ||||||||||||      |||      |||
Db     169 ATTATCTATGCCCTGGTATTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTC 228

Qy     125 LeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaVal 144
           :::|||      |||          |||   ||||||   :::||||||:::|||||||:::
Db     229 ATCTTATACAGCAGGGTCGGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTG 288

Qy     145 AlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrp 164
           ||||||   |||      ||||||||||||:::||||||                  |||
Db     289 GCCGACCTACTCTTTGCCCTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGG 348

Qy     165 ValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAla 184
           :::||||||:::   ||||||||||||        |||      :::||||||||||:::
Db     349 ATTTTTGGCACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGT 408

Qy     185 GlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThr 204
           |||   ||||||||||||||||||||   ||||||||||||   ||||||||||||||||
Db     409 GGCATCCTGCTACTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACA 468

Qy     205 GlnLeuTyrArgArgGlyProProAlaArgValThrLeuThr----------------- 218
           :::                          |||||||||
Db     469 CGC----------------------------ACACTGACCCAGAAGCGCTACTTGGTC 498

Qy     219 ---------CysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
                   ||||||::::::|||||||||   ||||||   |||||||||      :::
Db     499 AAATTCATATGTCTCAGCATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTT 558

Qy     236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
           |||           :::        ::::::         |||         :::
Db     559 TTCCGAAGGACCGTCTACTCATCCAATGTTAGCCCAGCC---TGC---------TATGAG 606

Qy     256 GlnValGly----------------ArgThrAlaLeuArgValLeuGlnLeuValAla 269
           :::|||                  |||      ||||||:::|||
Db     607 GACATGGGCAACAATACAGCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTT 666

Qy     270 GlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
           ||||||::::::|||||||||:::|||   :::||||||         |||      |||
Db     667 GGCTTCATCGTGCCACTGCTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTG 726

Qy     290 LeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValVal 309
               :::        ::::::   ||||||||||||::::::      ||||||:::
Db     727 TTTAAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTC 786

Qy     310 AlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAsp 329
           |||   |||||||||   ||||||:::||||||:::|||   |||   ||||||
Db     787 ATCTTCCTGCTTTGCTGGCTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGG 846

Qy     330 LeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
                  :::         |||   |||   :::   :::|||   |||
Db     847 ACCCAGGTGATCCAGGAGACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCC 906

Qy     350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
           |||       ||||||   :::|||   |||||||||||||||:::|||||||||:::|||
Db     907 ACCGAGATTCTGGGCATCCTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGC 966

Qy     370 ValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArg 389
           |||||||||       :::       :::|||          |||      ::::::
Db     967 CAGAAGTTTCGCCATGGACTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGAC 1026

Qy     390 GlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSer 408
           |||   :::                |||      ||||||      ||||||
Db    1027 TCCCTGCCCAAAGACAGCAGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1083


Search completed: November  2, 2002, 12:19:15
Job time : 242 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:27:35 ; Search time 1693 Seconds
(without alignments)
3308.468 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09101518/runat_29102002_091103_98/app_query.fasta_1.583
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09101518_@CGN_1_1_763_@runat_29102002_091103_98 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1251.5	58.2	851	10	BI768435	BI768435 603053902
	2	1236.5	57.5	864	10	BI911171	BI911171 603062744
	3	1153	53.6	749	10	BI821147	BI821147 603035039
	4	790	36.7	578	10	BI975807	BI975807 484335 MA
	5	739	34.4	471	9	AW655246	AW655246 106015 MA
	6	576	26.8	971	9	AU091121	AU091121 AU091121
	7	549.5	25.5	468	10	BF452722	BF452722 maa56a05.
	8	522	24.3	511	10	BE589641	BE589641 195994 BA
	9	514	23.9	3005	11	AK019478	AK019478 Mus muscu
	10	507	23.6	993	12	CNS043RI	AL273159 Tetraodon
	11	506	23.5	935	9	AL531903	AL531903 AL531903
	12	475.5	22.1	871	10	BI653693	BI653693 603300354
	13	466	21.7	392	9	AW354767	AW354767 36085 MAR
	14	460	21.4	944	9	AL523112	AL523112 AL523112
	15	452.5	21.0	910	10	BI762229	BI762229 603049139
	16	433	20.1	907	9	AL552677	AL552677 AL552677
	17	417.5	19.4	875	10	BI756157	BI756157 603030061
	18	413	19.2	905	10	BI754094	BI754094 603027651
	19	411.5	19.1	798	9	AU240364	AU240364 AU240364
	20	411.5	19.1	841	9	AL558854	AL558854 AL558854
c	21	411	19.1	708	10	BF453946	BF453946 maa56a05.
	22	408	19.0	827	10	BI761664	BI761664 603046395
	23	403.5	18.8	857	10	BG682791	BG682791 602651283
	24	392	18.2	891	10	BI824663	BI824663 603033815
	25	391.5	18.2	866	12	CNS02RNL	AL210810 Tetraodon
c	26	382.5	17.8	674	10	BM251350	BM251350 BOTL01000
	27	382.5	17.8	750	10	BG613352	BG613352 602641234
	28	381	17.7	913	10	BM051973	BM051973 603638877
	29	380.5	17.7	676	9	AJ398841	AJ398841 AJ398841
	30	380.5	17.7	746	10	BI917014	BI917014 603177688
	31	371.5	17.3	501	10	BG407320	BG407320 dab17c07.
	32	371.5	17.3	782	10	BG685901	BG685901 602638730
	33	367.5	17.1	702	10	BI761118	BI761118 603043593
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	35	366	17.0	733	9	AI959485	AI959485 fd10g03.y
	36	366	17.0	938	9	AL543359	AL543359 AL543359
	37	363	16.9	728	9	AU117058	AU117058 AU117058
	38	362.5	16.9	658	10	BI835125	BI835125 603087792
	39	362.5	16.9	703	10	BI765768	BI765768 603046522
	40	362.5	16.9	742	10	BI597875	BI597875 603245357
	41	361	16.8	671	10	BG025793	BG025793 602274794
c	42	359	16.7	573	10	BI395190	BI395190 TUDPEc185
	43	353	16.4	765	10	BM387369	BM387369 UI-R-CN1-
	44	351	16.3	853	9	AL561603	AL561603 AL561603
	45	348	16.2	561	10	BF591285	BF591285 7h44g03.x

ALIGNMENTS

RESULT 1
BI768435
LOCUS BI768435 851 bp mRNA linear EST 25-SEP-2001
DEFINITION 603053902F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203512 5', mRNA sequence.
ACCESSION BI768435
VERSION BI768435.1 GI:15760013
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11510 row: c column: 01

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          High quality sequence stop: 801.
FEATURES             Location/Qualifiers
     source          1. .851
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5203512"
                     /clone_lib="NIH_MGC_122"
                     /lab_host="DH10B"
                     /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                     Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                     anonymous pool of 24 week female lung, 16 week female
                     spleen, and 20-22 week male spleens.  Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon  cloning).  Average insert size 1.4 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was  constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking  code 026. Note:
                     this is a NIH_MGC Library."
BASE COUNT      128 a    305 c    240 g    178 t
ORIGIN

Alignment Scores:
Pred. No.:              5.24e-114      Length:         851
Score:                  1251.50        Matches:        262
Percent Similarity:     92.61%         Conservative:   1
Best Local Similarity:  92.25%         Mismatches:     14
Query Match:            58.18%         Indels:         9
DB:                     10             Gaps:           1

US-09-101-518A-2 (1-415) x BI768435 (1-851)

Qy      41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||            ||||||            :::|||||||||||||||
Db       7 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 66

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 126

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 186

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 246

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 306

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 366

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 426

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 486

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 546

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 606

Qy     237 LeuSerAlaHisHis-AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGl 256
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Db     607 CTGTCGGCCCACCAGCGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACA 666

Qy     256 nValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly-PheLeuLeuProLeuL 276
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     667 GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTTGCTGCCCCTGC 726

Qy     276 euValMetAlaTyrCysTyrAlaHisIleLeuAla-ValLeuLeuValSerArgGlyGln 295
           ||||||||||||||   ||||||||||||||||||| ||||||||||||||||||||||||
Db     727 TGGTCATGGCCTACTTGTATGCCCACATCCTGGCCTGTGCTGCTGGTTTCCAGGGGCCAG 786

Qy     296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
           ||||||||||||   ||||||   |||||||||            ||||||||   |||
Db     787 CGGCGCCTGCGGGC-ATGCGGCT-GTGGTGGTAGGCAGTGGTGGCTTTGCCCTCTGGTGG 844

Qy     316 ThrPro 317
           ||||||
Db     845 ACCCCC 850

RESULT 2
BI911171
LOCUS       BI911171                 864 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603062744F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212066 5',
            mRNA sequence.
ACCESSION   BI911171
VERSION     BI911171.1  GI:16174778
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11532  row: g  column: 11
            High quality sequence start: 3
            High quality sequence stop: 788.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated  adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      133 a    306 c    246 g    179 t
ORIGIN

Alignment Scores:
Pred. No.:              1.66e-112      Length:         864
Score:                  1236.50        Matches:        259
Percent Similarity:     92.61%         Conservative:   4
Best Local Similarity:  91.20%         Mismatches:     16
Query Match:            57.48%         Indels:         8
DB:                     10             Gaps:           1
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```
US-09-101-518A-2 (1-415) x BI911171 (1-864)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||           ||||||           :::|||||||||||||||||
Db      17 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 76

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 136

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 196

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 256

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 316

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 376

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 436

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 496

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 556

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     557 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 616

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db     617 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCAC-CACTGCCAATACAACTTCCCACAG 675

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 735

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db     736 GTCATGGCCTACTGCTATGC-CACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 794

Qy     297 -ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpTh 316
            ||||||:::||||||   |||                    ||||||:::   |||||
Db     795 GCGCCTGCAGGCCATGCTGCTTGGTGGTAGGGAGCCGGGTGGCTTTGCCGTCTG-TGGAC 853

Qy     316 rProTyrHis 319
           |||||||:::
Db     854 CCCTTATTAC 863

RESULT 3
BI821147
LOCUS       BI821147                749 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603035039F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176136 5',
            mRNA sequence.
ACCESSION   BI821147
VERSION     BI821147.1  GI:15932697
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11438  row: n  column: 09
            High quality sequence stop: 747.
FEATURES             Location/Qualifiers
     source          1. .749
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5176136"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      121 a    274 c    201 g    153 t
ORIGIN

Alignment Scores:
Pred. No.:              2.67e-104       Length:         749
Score:                  1153.00         Matches:        233
Percent Similarity:     94.35%          Conservative:   1
Best Local Similarity:  93.95%          Mismatches:     7
Query Match:            53.60%          Indels:         7
DB:                     10              Gaps:           1

US-09-101-518A-2 (1-415) x BI821147 (1-749)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||           ||||||           :::|||||||||||||||||
Db       6 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 65

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe-SerSerSerTyrAspTy 76
           ||||||||||||||||||||||||||||||||||||||||    |||||||||||||||
Db      66 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGGCTCTTCCTATGACTA 125

Qy      76 rGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLe 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 TGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCT 185

Qy      96 uAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLe 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 GAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCT 245

Qy     116 uGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAs 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 GGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGA 305

Qy     136 pThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTr 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     306 CACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTG 365

Qy     156 pAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAl 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db    366 GGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGC 425

Qy    176 aLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspAr 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 CCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCG 485

Qy    196 gTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValTh 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    486 CTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGAC 545

Qy    216 rLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePh 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    546 CCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTT 605

Qy    236 eLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGl 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    606 CCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACA 665

Qy    256 nValGlyArgThrAlaLeuArg-ValLeuGlnLeuValAla-GlyPheLeuLeuProLeu 275
          |||||||||||||||||||| |||||||||||||||||| |||||||||||||||||||
Db    666 GGTGGGCCGCACGGCTCTGCGGGGTGCTGCAGCTGGTGGCTTGGCTTTCTGCTGCCCCTG 725

Qy    276 LeuValMetAlaTyrCys 281
          |||||||||||   |||
Db    726 CTGGTCATGGCTAACTGT 743

RESULT 4
BI975807
LOCUS       BI975807                 578 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  484335 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI975807
VERSION     BI975807.1  GI:16350212
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 110  row: A  column: 16
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .578
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."

BASE COUNT       92 a    199 c    152 g    135 t
ORIGIN

Alignment Scores:
Pred. No.:                2.19e-68       Length:          578
Score:                    790.00         Matches:         153
Percent Similarity:       87.77%         Conservative:    12
Best Local Similarity:    81.38%         Mismatches:      21
Query Match:              36.73%         Indels:          2
DB:                       10             Gaps:            1

US-09-101-518A-2 (1-415) x BI975807 (1-578)

Qy     44 SerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAspAlaGluVal 63
          :::||||||            :::::::|||:::   |||            ::::::
Db     20 ACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGATTTT 79

Qy     64 AlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSer 83
          |||   ||||||||||||       ||||||||||||||||||||||||||:::
Db     80 GCCTACCTCCTGGAAAAC------TCTTCCTATGACTACGGAGAAAATGAGACCTACTTC 133

Qy     84 CysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeu 103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db    134 TGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTCCTG 193

Qy    104 ProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAla 123
          |||   ||||||||||||||||:::|||||||||||||||||||   ||||||
Db    194 CCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTGGGTAATGGCATCGTGGCAGTC 253

Qy    124 ValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAla 143
          ||||||||||||:::|||   ||||||||||||||||||||||||||||||||||||||
Db    254 GTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGACACCTTTCTGCTGCACTTGGCT 313

Qy    144 ValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGln 163
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db    314 GTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGGGCAGTGGATGCAGCCATCCAG 373

Qy    164 TrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyr 183
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    374 TGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCGGGTGCACTCTTCAACATCAACTTCTAC 433

Qy    184 AlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAla 203
          ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    434 GCAGGGGCCCTCCTGCTGGCCTGTATCAGCTTCGATCGGTACCTGAGCATTGTGCACGCC 493

Qy    204 ThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrp 223
          ||||||||||||||||||||||||   ||||||   |||||||||:::||||||||||
Db    494 ACCCAGCTCTACCGCCGGGGCCCCCCCGACTCGCGTGGCCCTCACCTGTGTGGCAGTCTGG 553

Qy    224 GlyLeuCysLeuLeuPheAlaLeu 231
          |||||||||||||||||||||||
Db    554 GGGCTCTGTCTGCTCTTTGCGCTC 577

RESULT 5
AW655246
LOCUS       AW655246                 471 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  106015 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW655246
VERSION     AW655246.1  GI:7421144
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
```

```
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 86  row: D  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT       72 a    152 c    148 g     99 t
ORIGIN

Alignment Scores:
Pred. No.:                1.88e-63       Length:          471
Score:                    739.00         Matches:         141
Percent Similarity:       95.48%         Conservative:    7
Best Local Similarity:    90.97%         Mismatches:      7
Query Match:              34.36%         Indels:          0
DB:                       9              Gaps:            0

US-09-101-518A-2 (1-415) x AW655246 (1-471)

Qy    244 ArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThrAlaLeuArg 263
          ||||||||||||||||||||||||||||||||||||||||   |||   ||||||||||||
Db      5 CGCCTCAATGCCACCCACTGCCAGTACAACTTCCCACAGGAGGGCCACACAGCTCTGCGC 64

Qy    264 ValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAla 283
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 ATCCTGCAGCTGGTGGCAGGCTTCCTGCTGCCCCTGCTGGTCATGGCCTATTGCTATGCC 124

Qy    284 HisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeu 303
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 CGCATCCTGGCTGTGCTGCTGGTCTCCAGGGGCCAGCGGCGGCTCAGAGCCATGCGGCTG 184

Qy    304 ValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeu 323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 GTGGTGGTGGTGGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTACCACCTGGTGGTGCTG 244

Qy    324 ValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgVal 343
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||   |||
Db    245 GTGGACACCCTCATGGACCTGGGGGCCTTAGCCCGTAACTGCGGCAGAGAAAGCAGTGTG 304

Qy    344 AspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu 363
          |||:::||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db    305 GACATAGCCAAGTCGGTCACGTCGGGCATGGGCTACATGCACTGCTGCCTCAACCCACTG 364

Qy    364 LeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeu 383
          ||||||||||||||||||||||||||||||||||||||||:::||||||:::||||||||
Db    365 CTCTATGCCTTTGTGGGTGTCAAGTTCCGAGAGCGGATGTGGGTGCTACTCGTGCGTCTG 424

Qy    384 GlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSer 398
          |||||||||:::||||||      |||||||||||||||:::|||
Db    425 GGCTGCCCTGACCAGAGGTGCCACCAGCGGCAGCCATCAGCTTCC 469

RESULT 6
AU091121
```

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LOCUS       AU091121                971 bp    mRNA    linear   EST 23-JAN-2001
DEFINITION  AU091121 lambda ZAPII-Con A stimulated leukocytes Paralichthys
            olivaceus cDNA clone JFConA882F forward similar to Gallus gallus
            Chemokine receptor-like protein (2412232A), mRNA sequence.
ACCESSION   AU091121
VERSION     AU091121.1  GI:12391161
KEYWORDS    EST.
SOURCE      bastard halibut.
  ORGANISM  Paralichthys olivaceus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
            Pleuronectoidei; Paralichthyidae; Paralichthys.
REFERENCE   1  (bases 1 to 971)
  AUTHORS   Nam,B., Hirono,I. and Aoki,T.
  TITLE     Identification of expressed genes from Japanese flounder
            (Paralichthys olivaceus) leukocytes stimulated with Con A/PMA
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Ikuo Hirono
            Laboratory of Genetics and Biochemistry
            Tokyo University of Fisheries
            Konan 4-5-7, Minato-ku, Tokyo 108, Japan
            Email: hirono@tokyo-u-fish.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .971
                     /organism="Paralichthys olivaceus"
                     /db_xref="taxon:8255"
                     /clone="JFConA882F"
                     /clone_lib="lambda ZAPII-Con A stimulated leukocytes"
                     /cell_type="leukocytes"
                     /dev_stage="adult"
BASE COUNT      205 a    248 c    221 g    297 t
ORIGIN

Alignment Scores:
Pred. No.:                9.13e-47       Length:          971
Score:                    576.00         Matches:         125
Percent Similarity:       55.83%         Conservative:    57
Best Local Similarity:    38.34%         Mismatches:      108
Query Match:              26.78%         Indels:          36
DB:                       9              Gaps:            8

US-09-101-518A-2 (1-415) x AU091121 (1-971)

Qy     70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
          ||||||:::      ||||||||||||   |||:::|||:::
Db     12 TTTTCCACGCCGACAGACTACGGAGAATATGAGAATGACACA----------------- 53

Qy     90 CysProGlnAspPheSer---------------------------------------- 95
                  |||:::|||
Db     54 ---------GACTATAGTCAACAGAACGTCTCCGACCTCCCAGTCTATATCTGTGAAGAA 104

Qy     96 --------------LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
                                                |||   |||   |||||||||||:::
Db    105 GAAGAGGAGCGCCTGCAGACCCTCGGCACTGTGTTCCAGCCTGTGTTGTACAGCTTGATC 164

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
          ||||||||||||:::::::|||||||||   :::      |||||||||   |||
Db    165 TTCCTGCTGGGTGTGGTAGGGAACGGCCTGATGATAACAGTCCTCCTGAGACGTTGGCGT 224

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
             |||      |||:::   :::|||||||||||||||:::||||||   :::|||:::
Db    225 CTCCTGCGCATCACTGAGATATACCTACTTCACCTCGCCCTGGCTGACCTCATGCTCCTT 284

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||   |||          ||||||            |||:::||||||      |||
Db    285 TTAACGTTCCCTTTCGATGTGGTCGACTTCGTCGCTGGTTGGTTGTTTGGGGATTTTCTC 344

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          ||||||:::   |||   :::   ::::::|||         |||:::   |||||||||
Db    345 TGCAAGCTGATGGGCCTGATGAAACATCTCAATCTCCTCTGTGGGAGTTTCCTTTTAGCT 404

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
```

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          ||||||   ||||||||||||||||   ||||||||||||           |||
Db    405 TGCATTGGGTTTGATCGGTATTTGGCTATCGTTCATGCCATTCCCAGCATGCGAAATCGG 464

Qy    211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
          |||      |||   :::|||||||:::   :::|||   :::||||||      :::
Db    465 CGTCCGAGAGCAGTGCATGTAACTTGCATTTTACTGTGGCTTGTCTGTTTGGGTTTATCA 524

Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGlu---ArgLeuAsnAlaThrHis 249
          |||:::|||:::|||||||||         ::::::         ::::::   :::
Db    525 GCTCCAAATTTTGTGTTTCTTTCTGTGAGAGAGGAGCAAACTAACACATCCAGCCTCTAC 584

Qy    250 CysGlnTyrAsnPheProGlnVal---GlyArgThrAlaLeu---------ArgValLeu 265
          |||   |||           :::   |||       :::          ||||||
Db    585 TGTCTCTATTATCATCATGACATCCATGGACACAACTGGGTTTTGACCAACAGAGTCTTC 644

Qy    266 GlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIle 285
          .     ::::::   |||   :::|||||   ||||||:::||||||||      :::
Db    645 GATCACATTTCC---TTTTTCGTACCTCTGGCTGTCATGAGCTACTGCTACACAGCAGTG 701

Qy    286 LeuAlaValLeuLeuValSer---ArgGlyGlnArgArgLeuArgAlaMetArgLeuVal 304
          :::      |||      |||   :::   |||::::::      ||||||||||||
Db    702 GTAGTTACTTTGTGCAACAGTCAGAAAAGCCAACAAAAGCAAGGAGCCATGCGACTGGCT 761

Qy    305 ValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuVal 324
          ::::::|||   :::   |||   |||||||||   ||||||::::::   :::|||:::
Db    762 TTACTTGTCAATCTTGTCTTTTGCCTCTGTTGGCTCCCATATAACATCACCTTACTGATA 821

Qy    325 AspIleLeuMetAspLeuGlyAlaLeu---AlaArgAsnCysGlyArgGluSerArgVal 343
                |||   ||||||      :::         :::|||         :::   :::
Db    822 AAAACTCTGTCAGACCTGGAGGTCATCCACTATGAAAGCTGTCAAACTTTTGCCCTGCTG 881

Qy    344 AspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeu 363
                |||      |||:::      |||||::::::|||||||||||||||||||||
Db    882 CGAGCCGCCCTCGATGTGTCCCTGAGTCTGGGATTCTTACACTGTTGCCTGAACCCCTTC 941

Qy    364 LeuTyrAlaPheValGly 369
          |||||||||||:::|||
Db    942 CTTTATGCCTTCATTGGG 959

RESULT 7
BF452722
LOCUS       BF452722                468 bp    mRNA    linear   EST 01-DEC-2000
DEFINITION  maa56a05.y1 Soares mouse 3NbMS Mus musculus cDNA clone
            IMAGE:3820689 5' similar to TR:O88410 O88410 CHEMOKINE RECEPTOR
            CXCR3. [1] ;, mRNA sequence.
ACCESSION   BF452722
VERSION     BF452722.1  GI:11518891
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1457041
            Seq primer: -40RP from Gibco
            High quality sequence stop: 382.
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3820689"
                     /clone_lib="Soares mouse 3NbMS"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
BASE COUNT       90 a    143 c    119 g    116 t
ORIGIN

Alignment Scores:
Pred. No.:              1.28e-44        Length:         468
Score:                  549.50          Matches:        112
Percent Similarity:     87.50%          Conservative:   7
Best Local Similarity:  82.35%          Mismatches:     16
Query Match:            25.55%          Indels:         1
DB:                     10              Gaps:           1

US-09-101-518A-2 (1-415) x BF452722 (1-468)

Qy     51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
          :::||||||:::   ||||||||||:::   ::::::   |||   ||||||||||||
Db     61 GAGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGC 120

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
          :::|||   ||||||||||||||||||||||||||          ||||||||||||
Db    121 ACCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGC 177

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db    178 CCACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTC 237

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
          |||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    238 TTCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACT 297

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
          |||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db    298 GCCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTG 357

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          |||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db    358 TTAACTCTTCCATTGTGGGCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCTTGCCTC 417

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAla 186
          ||||||||||||   ||||||||||||||||||||||||      |||
Db    418 TGCAAAGTGGCAAGCGCCTTGTTCAACATTAACTTTTATGTAAGGGCC 465

RESULT 8
BE589641
LOCUS       BE589641                511 bp    mRNA    linear   EST 28-AUG-2000
DEFINITION  195994 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BE589641
VERSION     BE589641.1  GI:9842680
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 511)
  AUTHORS   Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and
            Wells,K.D.
  TITLE     Mapping of Expressed Sequence Tags from a normalized bovine mammary
            gland cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Sonstegard TS
            USDA, ARS, Beltsville Agricultural Research Center
```

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           Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
           Tel: 301 504 8416
           Fax: 301 504 8414
           Email: tads@lpsi.barc.usda.gov
           Single pass sequencing. Bases called and alt_trimmed with phred
           v0.980904.e. Vector identified by cross_match with the -minscore 18
           and -minmatch 12 options.
           PCR PRimers
           FORWARD: AGGAAACAGCTATGACCAT
           BACKWARD: GTTTTCCCAGTCACGACG
           Plate: 122  row: N  column: 12
           Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .511
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="BARC 5BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT       97 a    167 c    135 g    112 t
ORIGIN

Alignment Scores:
Pred. No.:                7.95e-42        Length:          511
Score:                    522.00          Matches:         106
Percent Similarity:       81.56%          Conservative:    9
Best Local Similarity:    75.18%          Mismatches:      20
Query Match:              24.27%          Indels:          6
DB:                       10              Gaps:            2

US-09-101-518A-2 (1-415) x BE589641 (1-511)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||  ||||||           ||||||           ::::::|||:::   |||
Db      93 ACGCGGCCCAGCAGCCAGCGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAA 152

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
                  ::::::   |||   ||||||||||||      ||||||||||||||||
Db     153 GAGTTCCAAGCCTCCGATTTTGCCTACCTCCTGGAAAAC------TCTTCCTATGACTAC 206

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           |||||||||||:::       ||||||||||||||||||||||||||||||||||||||
Db     207 GGAGAAAATGAGACCTACTTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTC 266

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||  |||||||||  ||||||||||||||||:::||||||||||||
Db     267 AACTTCGACCGCACCTTCCTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTG 326

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           |||||||||  ||||||  ||||||||||||:::|||  ||||||||||||||||||
Db     327 GGTAATGGCATCGTGGCAGTCGTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGAC 386

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db     387 ACCTTTCTGCTGCACTTGGCTGTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGG 446

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db     447 GCAGTGGATGCAGCCATCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCGGGTGCA 506

Qy     177 Leu 177
           |||
Db     507 CTC 509

RESULT 9
AK019478
LOCUS       AK019478               3005 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
            library, clone:4632401H02:chemokine (C-C) receptor 10, full insert
            sequence.
ACCESSION   AK019478
VERSION     AK019478.1  GI:12859709
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:4632401H02.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 3005)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
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          prepared by using trehalose thermo-activated reverse transcriptase
          and subsequently enriched for full-length by cap-trapper. cDNA went
          through one round of normalization to Rot = 10.0 and subtraction to
          Rot = 100.0. Second strand cDNA was prepared with the primer
          adapter of sequence [5'
          GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
          with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was
          selected before cloning. Vector: a modified pBluescript KS(+) after
          bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
          end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
     source          1. .3005
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="MGD:MGI:1912190"
                     /db_xref="taxon:10090"
                     /clone="4632401H02"
                     /tissue_type="skin"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="0 day neonate"
     gene            296. .1405
                     /gene="Cmkbr10"
     CDS             296. .1405
                     /gene="Cmkbr10"
                     /note="chemokine (C-C) receptor 10
                     data source:MGD, source key:MGI:1341902, evidence:ISS
                     putative"
                     /codon_start=1
                     /protein_id="BAB31747.1"
                     /db_xref="GI:12859710"
                     /translation="MMPTELTSLIPGMFDDFSYDSTASTDDYMNLNFSSFFCKKNNVR
                     QFASHFLPPLYWLVFIVGTLGNSLVILVYWYCTRVKTMTDMFLLNLAIADLLFLATLP
                     FWAIAAAGQWMFQTFMCKVVNSMYKMNFYSCVLLIMCISVDRYIAIVQAMKAQVWRQK
                     RLLYSKMVCITIWVMAAVLCTPEILYSQVSGESGIATCTMVYPKDKNAKLKSAVLILK
                     VTLGFFLPFMVMAFCYTIIIHTLVQAKKSSKHKALKVTITVLTVFIMSQFPYNSILVV
                     QAVDAYAMFISNCTISTNIDICFQVTQTIAFFHSCLNPVLYVFVGERFRRDLVKTLKN
                     LGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL"
     polyA_signal    2981. .2986
                     /note="putative"
     polyA_site      3005
                     /note="putative"
BASE COUNT      814 a    734 c    648 g    809 t
ORIGIN

Alignment Scores:
Pred. No.:              7.55e-40        Length:         3005
Score:                  514.00          Matches:        112
Percent Similarity:     52.54%          Conservative:   74
Best Local Similarity:  31.64%          Mismatches:     142
Query Match:            23.90%          Indels:         26
DB:                     11              Gaps:           6

US-09-101-518A-2 (1-415) x AK019478 (1-3005)

Qy      69 AsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerPro 88
           ||||||||||||   :::
Db     389 AATTTCAGTAGCTTCTTC---------------------------------------- 406

Qy      89 ProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSer 108
              |||   ::::::            |||         |||||||||   ||||||
Db     407 ---TGTAAGAAAAATAATGTCAGGCAGTTTGCAAGCCATTTTCTTCCACCTCTGTACTGG 463

Qy     109 LeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArg 128
           |||:::|||::::::|||   |||||||||      |||      |||
Db     464 CTTGTGTTCATTGTGGGCACCTTGGGCAACAGCCTGGTCATCCTTGTCTACTGGTATTGC 523

Qy     129 ArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeu 148
                     :::   ||||||   |||||||||:::||||||:::||||||   |||
Db     524 ACAAGAGTGAAGACCATGACTGACATGTTCCTTTTGAATTTAGCCATTGCTGATCTGCTC 583

Qy     149 LeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySer 168
              :::   |||||||||   ||||||:::   ||||||   |||||||:::|||   :::
Db     584 TTTCTTGCCACTCTTCCCTTCTGGGCCATTGCTGCTGCTGGTCAATGGATGTTCCAGACC 643

Qy     169 GlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeu 188
              :::|||||||||      :::::::::   :::|||||||||:::      ||||||
Db     644 TTCATGTGCAAGGTTGTGAACAGCATGTACAAGATGAACTTCTACAGCTGTGTGCTTCTC 703

Qy     189 LeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAla------ThrGlnLeu 206
           :::   |||||||||   ||||||||||:::   ||||||   |||         |||:::
Db     704 ATCATGTGCATCAGTGTGGACAGATACATTGCCATTGTACAGGCCATGAAGGCTCAGGTC 763

Qy     207 TyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCys 226
           :::|||:::                  :::   |||:::   :::|||   :::
Db     764 TGGAGGCAGAAAAGGCTGCTATACAGCAAGATGGTCTGCATTACCATCTGGGTGATGGCA 823

Qy     227 LeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsn 246
              :::         |||:::   ::::::               :::      :::
Db     824 GCTGTGCTCTGCACCCCAGAAATCCTGTACAGTCAAGTCAGTGGGGAATCTGGTATT--- 880

Qy     247 AlaThrHisCysGlnTyrAsnPheProGlnValGly-----------ArgThrAlaLeu 262
           ||||||   |||         :::|||:::                 ::::::|||:::
Db     881 GCCACA---TGTACCATGGTCTACCCTAAGGATAAGAATGCCAAGCTAAAGTCAGCTGTC 937

Qy     263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
              :::|||::::::      ||||||   ||||||   :::||||||||||:::||||||
Db     938 TTGATCCTGAAGGTCACCTTGGGGTTTTCCTCCCCTTTATGGTCATGGCCTTCTGCTAT 997

Qy     283 AlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArg 302
                 |||:::      |||:::   ::::::         :::   :::|||::::::
Db     998 ACCATCATCATTCATACCTTGGTACAGGCCAAGAAGTCATCCAAGCACAAGGCCCTCAAG 1057

Qy     303 LeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuValVal 322
           :::   :::   |||:::      |||   :::   ::::::|||:::   ::::::
Db    1058 GTGACCATCACTGTCCTCACTGTCTTCATTATGTCTCAGTTCCCCTACAACTCCATTCTT 1117

Qy     323 LeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArg 342
           :::|||      :::                 ||||||         :::
Db    1118 GTAGTGCAGGCTGTTGACGCTTATGCCATGTTCATCTCCAACTGCACTATTTCCACCAAT 1177

Qy     343 ValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnPro 362
           :::|||:::         ||||||      :::   :::   |||   ||||||||||||
Db    1178 ATTGACATCTGCTTCCAGGTTACTCAGACTATTGCATTCTTCCACAGTTGTCTGAACCCA 1237

Qy     363 LeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeuArg 382
           :::||||||   |||||||||   :::||||||      :::         |||
Db    1238 GTTCTCTATGTTTTTGTTGGCGAGAGATTCCGAAGGGATCTGGTGAAGACCCTGAAGAAC 1297

Qy     383 LeuGlyCysProAsnGlnArg---------GlyLeuGlnArgGlnProSerSerSerArg 399
           |||||||||   :::|||                |||:::      |||   :::
Db    1298 CTGGGATGCATTAGCCAGGCCCAGTGGGTTTCATTCACAAGGAGAGAGGGTAGCTTGAAG 1357

Qy     400 ArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSer 413
                 |||         ||||||:::      :::   |||
Db    1358 CTTTCTTCTATGCTACTGGAGACAACTTCGGGGGCTCTCTCC 1399

RESULT 10
CNS043RI
LOCUS       CNS043RI                993 bp    DNA     linear   GSS 18-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            080013 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL273159
VERSION     AL273159.1  GI:7995408
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
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            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 993)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="080O13"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG080AH07SP1-end :
                     PUC-Ori"
BASE COUNT      223 a    275 c    232 g    258 t      5 others
ORIGIN

Alignment Scores:
Pred. No.:              6.84e-40        Length:         993
Score:                  507.00          Matches:        123
Percent Similarity:     51.08%          Conservative:   43
Best Local Similarity:  37.85%          Mismatches:     84
Query Match:            23.57%          Indels:         79
DB:                     12              Gaps:           5

US-09-101-518A-2 (1-415) x CNS043RI (1-993)

Qy    135 ThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuPro 154
          |||   ||||||:::|||||||||||||:::||||||   ||||||   :::|||||||||
Db      7 ACCGNCACCTTCATCCTCCACCTGGCAATGGCCGACGTGCTGCTAMTGGTGACTCTGCCC 66

Qy    155 LeuTrpAlaValAspAlaAlaValGln------TrpValPheGlySerGlyLeuCysLys 172
            ||||||      |||              |||   ||||||:::   |||||||||
Db     67 ACTTGGGCCGCACAGGCACCCAG-GATGAGGGCTGGACCTTCGGCACGCCTCTCTGCAAG 125

Qy    173 ValAlaGlyAlaLeuPhe---------------------------------------- 178
          :::   ||||||:::|||
Db    126 ATCACCGGAGCTGTTTTTATGGTAAGAAGTGCAGACGTAGGAAAACTGCAGCAAAGGGTT 185

Qy    178 ---------------------------------------------------------- 178

Db    186 TAATCTTCAATGATAGAAGCATTTTAACACTCCTTTAAGCCTTTAACACTCAAATCAAAA 245

Qy    179 ----------------------------------------------------------Asn 179
                                                                       :::
Db    246 TGAAAATAATGCATTTTAAGGTCACCCATTAAAAGATAATGTATGTTTCCTATGCCATCA 305

Qy    180 -IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAs 199
           :::|||||||||   |||      ||||||   ||||||||||||||||||||||||::
Db    306 GGTCAACTTCTACTGTGGGATTTTTCTCCTGGGCTGCATCAGTTTCGACCGGTACCTGTC 365

Qy    199 nIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCy 219
          :|||||||||||||   :::|||              |||      :::   ::::::||
Db    366 TATTGTCCATGCCACCCACATGTACTCCCACAGAAAGCCCTGGGCCATTCGGATCAGCTG 425

Qy    219 sLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAl 239
          |:::|||   |||        ||||||   ::::::   |||   :::|||||   ||
Db    426 CATGGCTGCCTGGCTTTTCTCCCTACTGCTCTCCATTACAGACCTGGTCTTTCTAGAAGC 485

Qy    239 aHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnVal----- 257
          |      |||:::|||||||||   |||   |||      |||:::      |||
Db    486 TGTGAGCGATGATAGACTGAACCGAACAATGTGCTTTCGTAACTATTT-AATGTTCACGA 544

Qy    258 ----------------------------------------------GlyArgThrAlaLe 262
                                                           :::   |||
Db    545 AGCAATCCGAAGAGTTCACCGCAGCGTTAATTCGACGCAGGTTAACTGGCAGCTGGCATC 604

Qy    262 uArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTy 282
           |||::::::      :::   ||||||||||||||      ||||||   :::|||||
Db    605 GCGGCTGATCTACCACCTAGTGGGTTTCCTCTTGCCCTCAGCCGTCATGATCTTCTGCTA 664

Qy    282 rAlaHisIleLeuAlaValLeu---LeuValSerArgGlyGlnArgArgLeuArgAlaMe 301
          |      ||||||      |||         |||:::|||   ::::::   ||||||::
Db    665 CACCTGCATCCTGCGTCGGCTGAGGTGCAGCTCGCAGGGCCTTCAAAAGCAGAGAGCTAT 724

Qy    301 tArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVa 321
          :|||:::::::::   ||||||      |||   ||||||||||||||||||:::::||
Db    725 CAGGGTGATCATCGCTGTGGTGGCGGTGTTTTTCCTCTGCTGGACGCCCTACAACATCGT 784

Qy    321 lValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSe 341
          |:::|||||||||                        :::      ||||||      ::
Db    785 CCTCCTGGTGGACACGTTTTACTCTCCCAGTGGC---AGTGATAAGTGTGGAATGCACAC 841

Qy    341 rArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAs 361
          :   ::::::   |||   :::||||||||||   :::||||||:::||||||   |||||
Db    842 ATCTATGGAGAAAGCCTTGACGGTAACCTCCTCCGTGGGTTACCTCCACTGCAGCCTCAA 901

Qy    361 nProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLe 381
          ||||:::||||||||||||||||||||||   ||||||         |||   :::|||
Db    902 CCCCATCCTGTATGCCTTCGTGGGGGTMAR-TTCAGGCGTCACTCCTGGCC-GTCCTGAG 959

Qy    381 uArgLeuGlyCys 385
            |||||||||
Db    960 GTCTCTGGGCTGT 972

RESULT 11
AL531903
LOCUS       AL531903                935 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL531903 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM003YH06 5
            prime, mRNA sequence.
ACCESSION   AL531903
VERSION     AL531903.1  GI:12795396
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DM003YH06"
                     /clone_lib="LTI_NFL001_NBC4"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      191 a    261 c    232 g    250 t      1 others
```

```
ORIGIN

Alignment Scores:
Pred. No.:              7.84e-40        Length:         935
Score:                  506.00          Matches:        119
Percent Similarity:     51.69%          Conservative:   34
Best Local Similarity:  40.20%          Mismatches:     97
Query Match:            23.52%          Indels:         46
DB:                     9               Gaps:           7

US-09-101-518A-2 (1-415) x AL531903 (1-935)

Qy      78 GluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPhe---SerLeu 96
           |||   |||   |||           :::   |||         ||||||      |||
Db      50 GAAACTGAAGAGGACATGTCAAATATTACAGATCCACAGATGTGGGATTTTGATGATCTA 109

Qy      97 AsnPhe-----------------AspArgAlaPheLeuProAlaLeu------------ 106
           ||||||               |||      :::   |||   :::
Db     110 AATTTCACTGGCATGCCACCTGCAGATGAAGATTACAGCCCCTGTATGCTAGAAACTGAG 169

Qy     107 ----------------------------TyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
                                       |||:::|||:::|||||||||   ||||||
Db     170 ACACTCAACAAGTATGTTGTGATCATCGCCTATGCCCTAGTGTTCCTGCTGAGCCTGCTG 229

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||      |||      |||:::|||      |||         |||   ||||||
Db     230 GGAAACTCCCTGGTGATGCTGGTCATCTTATACAGTAGGGTCGGCCGCTCCGTCACTGAT 289

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           :::||||||:::||||||:::|||||   |||      ||||||||||||:::|||
Db     290 GTCTACCTGCTGAACCTGGCCTTGGCCGACCTACTCTTTGCCCTGACCTTGCCCATCTGG 349

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           |||                |||:::||||||::   ||||||||||
Db     350 GCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTGTGCAAGGTGGTCTCACTC 409

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           |||      :::|||||||||:::|||   ||||||||||||||||||||   ||||||
Db     410 CTGAAGGAAGTCAACTTCTACAGTGGCATCCTGCTGTTGGCCTGCATCAGTGTGGACCGT 469

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||   ||||||||||||||::                              |||
Db     470 TACCTGGCCATTGTCCATGCCACACGC----------------------------ACA 499

Qy     217 LeuThr--------------------------CysLeuAlaValTrpGlyLeuCysLeu 227
           ||||||                        ||||||      |||||||||   :::
Db     500 CTGACCCAGAAGCGTCACTTGGTCAAGTTTGTTTGTCTTGGCTGCTGGGGACTGTCTATG 559

Qy     228 LeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAla 247
                :::||||||   |||:::|||      |||:::|||         |||:::
Db     560 AATCTGTCCCTGCCCTTCTTCCTTTTCCGCCAGGCTTACCATCCAAAC------AATTCC 613

Qy     248 ThrHisCysGlnTyr------------AsnProGlnValGlyArgThrAlaLeuArg 263
           :::         |||           |||              |||      ||||||
Db     614 AGTCCAGTTTGCTATGAGGTCCTGGGAAATGACACAGCAAAATGGCGGATGGTGTTGCGG 673

Qy     264 ValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAla 283
           :::|||            ||||||:::::||||||   ||||||   :::||||||
Db     674 ATCCTGCCTCACACCTTTGGCTTCATCGTGCCGCTGTTTGTCATGCTGTTCTGCTATGGA 733

Qy     284 HisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeu 303
               |||      |||      :::       ::::::   ||||||||||||:::
Db     734 TTCACCCTGCGTACACTGTTTAAGGCCCACATGGGGCAGAAGCACCGAGCCATGAGGGTC 793

Qy     304 ValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeu 323
           :::      ||||||:::   |||   |||||||||   ||||||:::||||||:::|||
Db     794 ATCTTTGCTGTCGTCCTCATCTTCCTGCTTTGCTGGCTGCCCTACAACCTGGTCCTGCTG 853

Qy     324 ValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArg 339
           |||   ||||||           :::         |||   |||
Db     854 GCAGACACCCTCATGAGGACCCAGGTGATCCAGGAGACCTGTGAGCGC 901

RESULT 12
```

```
BI653693
LOCUS       BI653693                871 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603300354F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5340828 5',
            mRNA sequence.
ACCESSION   BI653693
VERSION     BI653693.1  GI:15567929
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11865  row: 1  column: 13
            High quality sequence stop: 835.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5340828"
                     /clone_lib="NIH_CGAP_Mam3"
                     /tissue_type="tumor, gross tissue"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert 2 kb. Library constructed by Life
                     Technologies, catalog #12017-018. Investigators providing
                     samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
                     for transgenic model: Xu et al., Nature Genetics 22, 37-43
                     (1999). Note: this is a NCI_CGAP Library."
BASE COUNT      164 a    274 c    221 g    212 t
ORIGIN

Alignment Scores:
Pred. No.:              7.57e-37        Length:         871
Score:                  475.50          Matches:        105
Percent Similarity:     56.58%          Conservative:   54
Best Local Similarity:  37.37%          Mismatches:     115
Query Match:            22.11%          Indels:         8
DB:                     10              Gaps:           3

US-09-101-518A-2 (1-415) x BI653693 (1-871)

Qy     135 ThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuPro 154
           |||||||||:::||||||:::||||||||||||||||   |||   :::|||   ||||||
Db       1 ACGGATACCTACCTGCTCAACCTGGCCGTGGCAGACATCCTTTTCCTCCTGATTCTTCCC 60

Qy     155 LeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAla 174
              ||||||         |||      |||:::||||||      |||||||||
Db      61 TTCTGGGCCTACAGCGAAGCCAAGTCCTGGATCTTTGGCGTCTACCTGTGTAAGGGCATC 120

Qy     175 GlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPhe 194
                  ::::::   ::::::|||::::::|||   |||||||||   |||||||||
Db     121 TTTGGCATCTATAAGTTAAGCTTCTTCAGCGGGATGCTGCTGCTCCTATGCATCAGCATT 180

Qy     195 AspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArg 214
           ||||||||||:::   ||||||   |||         :::|||           ||||||
Db     181 GACCGCTACGTAGCCATCGTCCAGGCCGTGTCGGCTCATCGCCAC------CGCGCCCGC 234

Qy     215 Val------------ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
           |||               |||:::|||:::   :::|||   |||   |||      :::
Db     235 GTGCTTCTCATCAGCAAGCTGTCCTGTGTGGGCATCTGGATGCTGGCCCTCTTCCTCTCC 294
```

```
Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
          :::|||:::   ::::::               :::         :::         |||
Db    295 ATCCCGGAGCTGCTCTACAGCGGCCTCCAGAAGAACAGCGGCGAGGACACGCTGAGATGC 354

Qy    251 GlnTyrAsnPheProGlnVal---GlyArgThrAlaLeuArgValLeuGlnLeuValAla 269
                      ||||||          :::::|||   |||:::|||
Db    355 TCACTGGTCAGTGCCCAAGTGGAGGCCTTGATCACCATCCAAGTGGCCCAGATGGTTTTT 414

Qy    270 GlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu 289
          |||||||||:::|||:::|||   |||:::::|||||      |||:::      |||
Db    415 GGGTTCCTAGTGCCTATGCTGGCTATGAGTTTCTGCTACCTCATTATCATCCGTACCTTG 474

Qy    290 LeuValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValVal 309
          |||   :::|||         |||   :::|||:::::::::::::::   |||||||||
Db    475 CTCCAGGCACGCAACTTTGAGCGGAACAAGGCCATCAAGGTGATCATTGCCGTGGTGGTA 534

Qy    310 AlaPheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAsp 329
          |||   :::         ||||||:::   |||||||||         :::   :::
Db    535 GTCTTCATAGTCTTCCAGCTGCCCTACAATGGGGTGGTCCTGGCTCAGACGGTGGCCAAC 594

Qy    330 LeuGlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerVal 349
                    :::|||           :::::::::::|||      |||
Db    595 TTCAACATCACCAATAGCAGCTGCGAAACCAGCAAGCAGCTCAACATTGCCTATGACGTC 654

Qy    350 ThrSerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGly 369
          |||       |||       :::   ||||||:::||||||   |||||||||||:::|||
Db    655 ACCTACAGCCTGGCCTCCGTCCGCTGCTGCGTCAACCCTTTCTTGTATGCCTTCATCGGC 714

Qy    370 ValLysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArg 389
          ||||||||||||      ::::::   |||       ||||||      :::   |||
Db    715 GTCAAGTTCCGCAGCGACCTCTTCAAGCTCTTCAA-GGACTTGGGGCTGTCTCAGCCAGG 773

Qy    390 GlyLeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGlu 409
                |||       ||||||   |||         :::   |||   :::   |||
Db    774 AACGGCTCCCGGCACTGGTCTTCCTGCCGGCATGTACGGAACGCGTCGGTGAGCATTGAG 833

Qy    410 Ala 410
          |||
Db    834 GCG 836
```

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RESULT 13
AW354767
LOCUS       AW354767                392 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  36085 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW354767
VERSION     AW354767.1  GI:6853757
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 23  row: J  column: 5
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES    Location/Qualifiers
     source 1. .392
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /clone_lib="MARC 1BOV"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
            Library made from pooled tissue from lymph node, ovary,
            fat, hypothalamus, and pituitary."
BASE COUNT      70 a    131 c    102 g     89 t
ORIGIN
```

```
Alignment Scores:
Pred. No.:                1.95e-36        Length:          392
Score:                    466.00          Matches:         95
Percent Similarity:       80.00%          Conservative:    9
Best Local Similarity:    73.08%          Mismatches:      20
Query Match:              21.66%          Indels:          6
DB:                       9               Gaps:            2

US-09-101-518A-2 (1-415) x AW354767 (1-392)

Qy     41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
          |||   ||||||            ||||||           ::::::|||:::   |||
Db      8 ACGCGGCCCAGCAGCCAGCGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAA 67

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
                  ::::::   |||   ||||||||||||      ||||||||||||||||
Db     68 GAGTTCCAAGCCTCCGATTTTGCCTACCTCCTGGAAAAC------TCTTCCTATGACTAC 121

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
          ||||||||||||:::      ||||||||||||||||||||||||||||||||||||||
Db    122 GGAGAAAATGAGACCTACTTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTC 181

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
          ||||||||||||   |||||||||   ||||||||||||||||||:::||||||||||||
Db    182 AACTTCGACCGCACCTTCCTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTG 241

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
          |||||||||   ||||||   ||||||||||||:::|||   ||||||||||||||||||
Db    242 GGTAATGGCATCGTGGCAGTCGTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGAC 301

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
          ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db    302 ACCTTTCTGCTGCACTTGGCTGTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGG 361

Qy    157 AlaValAspAlaAlaValGlnTrpValPhe 166
          |||||||||||||||:::|||||||||||
Db    362 GCAGTGGATGCAGCCATCCAGTGGGTCTTT 391
```

```
RESULT 14
AL523112
LOCUS       AL523112                944 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL523112 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YB09 5
            prime, mRNA sequence.
ACCESSION   AL523112
VERSION     AL523112.1  GI:12786605
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 944)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
```

```
           BP 191 91006 EVRY cedex - France
           Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .944
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DC001YB09"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      106 a    357 c    301 g    174 t      6 others
ORIGIN

Alignment Scores:
Pred. No.:              2.98e-35       Length:         944
Score:                  460.00         Matches:        121
Percent Similarity:     53.19%         Conservative:   29
Best Local Similarity:  42.91%         Mismatches:     124
Query Match:            21.39%         Indels:         9
DB:                     9              Gaps:           2

US-09-101-518A-2 (1-415) x AL523112 (1-944)

Qy      98 PheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGly 117
           |||   |||||||||   |||:::::::         :::      |||||||||   |||
Db      52 TTCAGCCGGGCCTTCCAACCCAGTGTCTCCCTGACCGTGGCTGCGCTGGGTCTGGCCGGC 111

Qy     118 AsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeu-SerSerThrAspTh 137
           ||||||   |||   |||      |||:::   |||   |||    |||   |||
Db     112 AATGGCCTGGTCCTGGCCACCCACCTGGCAGCCCGACGCGCAGCGCTCGCCCACCTCTGC 171

Qy     137 rPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAl 157
               ||||||   ||||||:::||||||   ||||||   ||||||||||||      ||
Db     172 CCACCTGCTCCAGCTGGCCCTGGCCGACCTCTTGCTGGCCCTGACTCTGCCCTTCGCGGC 231

Qy     157 aValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLe 177
           |      |||         |||      ||||||      |||:::           ||
Db     232 AGCAGGGGCTCTTCAGGGCTGGAGTCTGGGAAGTGCCACCTGCCGCACCATCTCTGGCCT 291

Qy     177 uPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTy 197
           |:::::   :::|||:::||||||   |||   ||||||||||||||   ||||||||
Db     292 CTACTCGGCCTCCTTCCACGCCGGCTTCCTCTTCCTGGCCTGTATCAGCGCCGACCGCTA 351

Qy     197 rLeuAsnIleValHisAlaThrGlnLeuTyr-ArgArgGlyProProAlaArgValThrL 217
           |:::   |||                  |||         |||   |||      |
Db     352 CGTGGCCATCGCGCGAVCTCCCAGCCGGGCCGCGGCCCTCCACTCCCGGCCGCGCACACT 411

Qy     217 euThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheL 237
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Db     412 TGGTCTCCGTCATCGTGTGGCTGCTGTAACTGCTCCTGGCGCTGCCTGCGCTGCTCTTC- 470

Qy     237 euSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro---- 255
               :::         :::|||               |||:::   |||||||||
Db     471 -----AGCCAGGATGGGCAGCGGGAAGGCCAACGACGCTGTCGCCTCAACTTCCCCGAGG 525

Qy     256 --------GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuL 273
                   |||      :::   |||      |||   ::::::      ||||||   |
Db     526 GCCTCACGCAGACGGTGAAGGGGGCGAGCGCCGTGGCSAGGGTGGCCCTGGGCTTCGCGC 585

Qy     273 euProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerA 293
           ||||||||   ||||||      |||||||||   :::         ||||||   :::|
Db     586 TGCCGCTGGGCGTCATGGTAGCCTGCTACGCGCTTCTGGGCCGCACGCTGCTGGCCGCCA 645
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Qy     293 rgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaL 313
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Db     646 GGGGGCCCGAGCGCCGGCGTGCGCYGCGCGTCGTGGTGGCTCTGGTGGCGGCCTTCGTGG 705

Qy     313 euCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaL 333
           ::         ||||||   |||   :::|||:::|||            |||   |||
Db     706 TGCTGCAGCYGCCCTACAGCCTCGCCCTGCTGCTGGATACTGCCGATCTACTGGCTGCGC 765

Qy     333 euAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyL 353
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Db     766 GCGAGGGAGCTGCCCCTGCCAGCAAACGCAAGGATGTCGCACTGCTGGTGACCAGCGGCT 825

Qy     353 euGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheA 373
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Db     826 TGGCCCTCGCCCGCTGTGGCCTCAATCCCGTKCTCTACGCTTTCTG-GGCCTGCGCTTCC 884

Qy     373 rg 373
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Db     885 GC 886

RESULT 15
BI762229
LOCUS       BI762229                910 bp    mRNA    linear   EST 25-SEP-2001
DEFINITION  603049139F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5189552 5',
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ACCESSION   BI762229
VERSION     BI762229.1  GI:15753807
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11473  row: m  column: 09
            High quality sequence stop: 827.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female.  Library is
                     oligo-dT primed and  directionally cloned (EcoRV site is
                     destroyed upon cloning).  Average insert size 1.4 kb,
                     insert size range 1-3 kb.  Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber  (Invitrogen).  Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."
BASE COUNT      210 a    260 c    208 g    232 t
ORIGIN

Alignment Scores:
Pred. No.:              1.57e-34       Length:         910
Score:                  452.50         Matches:        101
Percent Similarity:     56.47%         Conservative:   56
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Best Local Similarity:  36.33%          Mismatches:     109
Query Match:            21.04%          Indels:         12
DB:                     10              Gaps:           5

US-09-101-518A-2 (1-415) x BI762229 (1-910)

Qy      62 GluValAlaAlaLeuLeuGluAsnPheSer------SerSerTyrAspTyr--------- 76
           |||   |||      :::|||      |||      :::|||   :::|||
Db      59 GAACCAGCGGTTACCATGGAGGGGATCAGTATATACACTTCAGATAACTACACCGAGGAA 118

Qy      77 ---GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
              |||      :::   ||||||               ||||||   ::::::   :::
Db     119 ATGGGCTCAGGGGACTATGACTCC------ATGAAGGAACCCTGTTTCCGTGAAGAAAAT 172

Qy      96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
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Db     173 GCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTCCATCATCTTCTTAACTGGCATT 232

Qy     116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
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Db     233 GTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGAAGCATGACG 292

Qy     136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
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Db     293 GACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACGCTTCCCTTC 352

Qy     156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
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Db     353 TGGGCAGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCAT 412

Qy     176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
           ::::::   :::|||   |||:::      |||:::||||||   ||||||   |||
Db     413 GTCATCTACACAGTCAACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGAC 472

Qy     196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
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Db     473 CGCTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGCTGTTGGCTGAA 532

Qy     216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
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Qy     236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
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Db     593 TTT------GCCAACGTCAGTGAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCC 646

Qy     256 ---GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuPro 274
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Db     647 AATGACTTGTGGGTGGTTGTGTACCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCT 706

Qy     275 LeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGly 294
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Qy     295 GlnArgArgLeuArgAlaMetArgLeuValValValValValAlaPhe-AlaLeuCy 314
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Db     767 CACCAGAAGCGCCAGGCCCTCCAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCCTG 826

Qy     314 sTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
           ||||   ||||||:::      :::   ::::::   |||         |||
Db     827 TTGGCTGCCTTACTACTTTGGGATCAGCATCGAATTCCTTTCACCTCCTGGA 878

Search completed: November  2, 2002, 14:15:58
Job time : 1706 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:19:26 ; Search time 2890 Seconds
(without alignments)
3106.742 Million cell updates/sec

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Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

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Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2142	99.6	1876	1	PCT-US96-00499A-1	Sequence 1, Appli
	3	2142	99.6	1876	15	US-09-101-518-1	Sequence 1, Appli
	4	2136	99.3	1877	1	PCT-US00-26524B-2115	Sequence 2115, Ap
c	5	2116	98.4	6604	64	US-60-258-273-3	Sequence 3, Appli
	6	2073	96.4	1293	14	US-09-016-434-1052	Sequence 1052, Ap
	7	2073	96.4	1293	36	US-09-960-706-962	Sequence 962, App
	8	1897	88.2	1670	14	US-09-023-655-980	Sequence 980, App
	9	1897	88.2	1670	24	US-09-624-594-1	Sequence 1, Appli
	10	1897	88.2	1670	24	US-09-633-541-1	Sequence 1, Appli
	11	1897	88.2	1670	26	US-09-663-702-1	Sequence 1, Appli
	12	1897	88.2	1670	26	US-09-663-799-1	Sequence 1, Appli
	13	1897	88.2	1670	33	US-09-880-107-3833	Sequence 3833, Ap
	14	1891	87.9	1107	15	US-09-170-496-19	Sequence 19, Appl
	15	1891	87.9	1107	15	US-09-170-496C-19	Sequence 19, Appl
	16	1891	87.9	1107	15	US-09-170-496D-19	Sequence 19, Appl

	17	1885	87.6	1107	15	US-09-170-496C-173 Sequence 173, App
	18	1885	87.6	1107	15	US-09-170-496D-173 Sequence 173, App
	19	1875	87.2	1626	64	US-60-258-273-211 Sequence 211, App
	20	1632.5	75.9	1608	75	US-60-360-207-302 Sequence 302, App
	21	1627.5	75.7	1620	14	US-09-010-701C-21 Sequence 21, Appl
	22	1595	74.2	2914	60	US-60-212-655-911 Sequence 911, App
	23	1515.5	70.5	1024	27	US-09-699-011A-485 Sequence 485, App
	24	1451	67.5	2836	61	US-60-229-515-1618 Sequence 1618, Ap
	25	1342	62.4	814	60	US-60-213-169-650 Sequence 650, App
	26	1342	62.4	814	60	US-60-213-170-650 Sequence 650, App
	27	1302.5	60.6	965	60	US-60-213-844-16 Sequence 16, Appl
c	28	1066	49.6	615	37	US-10-029-386-25025 Sequence 25025, A
c	29	1034	48.1	600	37	US-10-029-386-3624 Sequence 3624, Ap
c	30	878	40.8	503	37	US-10-029-386-11311 Sequence 11311, A
	31	821	38.2	628	60	US-60-213-844-494 Sequence 494, App
	32	782	36.4	560	27	US-09-698-013-414 Sequence 414, App
	33	756.5	35.2	519	27	US-09-698-013-1151 Sequence 1151, Ap
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	36	643	29.9	2518	75	US-60-360-207-6145 Sequence 6145, Ap
	37	640.5	29.8	1068	1	PCT-US01-16777-47 Sequence 47, Appl
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	39	640	29.8	2517	36	US-09-997-722-158 Sequence 158, App
	40	639.5	29.7	1068	1	PCT-US01-16777-48 Sequence 48, Appl
	41	639	29.7	1402	61	US-60-229-515-1889 Sequence 1889, Ap
	42	637.5	29.6	1777	59	US-60-209-009-227 Sequence 227, App
	43	637.5	29.6	1886	1	PCT-US01-03800A-1044 Sequence 1044, Ap
	44	637.5	29.6	1886	18	US-09-496-914A-8718 Sequence 8718, Ap
	45	637.5	29.6	1886	22	US-09-560-875A-8718 Sequence 8718, Ap

ALIGNMENTS

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RESULT 1
PCT-US96-00499-1
; Sequence 1, Application PC/TUS9600499
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;    TITLE OF INVENTION:  HSATU68
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00499
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-474
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  173..1417
PCT-US96-00499-1

Alignment Scores:
Pred. No.:              2.14e-191     Length:          1876
Score:                  2142.00       Matches:         414
Percent Similarity:     99.76%        Conservative:    0
Best Local Similarity:  99.76%        Mismatches:      1
Query Match:            99.58%        Indels:          0
DB:                     1             Gaps:            0

US-09-101-518A-2 (1-415) x PCT-US96-00499-1 (1-1876)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
           |||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db     473 GCCTTCCTGCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy     121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy     141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 CACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy     161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy     181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy     201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy     221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy     241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy     261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy     281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072
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Qy     301 MetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
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Db    1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy     321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy     341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy     361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy     381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy     401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 2
PCT-US96-00499A-1
; Sequence 1, Application PC/TUS9600499A
;  GENERAL INFORMATION:
;     APPLICANT:  LI, Yi
;     TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;     TITLE OF INVENTION:  HSATU68
;     NUMBER OF SEQUENCES:  9
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;       ADDRESSEE:  Stewart & Olstein
;       STREET:  6 Becker Farm Road
;       CITY:  Roseland
;       STATE:  NJ
;       COUNTRY:  USA
;       ZIP:  07068-1739
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US96/00499A
;       FILING DATE:  11 JAN 1996
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MULLINS, J.G.
;       REGISTRATION NUMBER:  33,073
;       REFERENCE/DOCKET NUMBER:  325800-474
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1876 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  173..1417
PCT-US96-00499A-1

Alignment Scores:
Pred. No.:              2.14e-191      Length:         1876
Score:                  2142.00        Matches:        414
Percent Similarity:     99.76%         Conservative:   0
Best Local Similarity:  99.76%         Mismatches:     1
Query Match:            99.58%         Indels:         0
DB:                     1              Gaps:           0

US-09-101-518A-2 (1-415) x PCT-US96-00499A-1 (1-1876)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
           |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db     473 GCCTTCCTGCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy     121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy     141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 CACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy     161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy     181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy     201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy     221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy     241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy     261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy     281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy     301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy     321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192
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Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 3
US-09-101-518-1
; Sequence 1, Application US/09101518
; GENERAL INFORMATION:
;  APPLICANT:  Li, Yi
;  TITLE OF INVENTION:  Human G-Protein Chemokine Receptor HSATU68
;  FILE REFERENCE:  PF218PCT.US
;  CURRENT APPLICATION NUMBER: US/09/101,518
;  CURRENT FILING DATE:  1998-12-21
;  PRIOR APPLICATION NUMBER:  PCT/US96/00499
;  PRIOR FILING DATE:  1996-01-11
;  NUMBER OF SEQ ID NOS:  9
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1876
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (173)..(1420)
US-09-101-518-1

Alignment Scores:
Pred. No.:              2.14e-191      Length:          1876
Score:                  2142.00        Matches:         414
Percent Similarity:     99.76%         Conservative:    0
Best Local Similarity:  99.76%         Mismatches:      1
Query Match:            99.58%         Indels:          0
DB:                     15             Gaps:            0

US-09-101-518A-2 (1-415) x US-09-101-518-1 (1-1876)

Qy      1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy     21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy     41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy     61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy     81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
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Db    413 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy    101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
          ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db    473 GCCTTCCTGCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy    121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy    141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 CACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy    161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy    181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
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Db    713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy    201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
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Db    773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy    221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGlnValGlyArgThr 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy    261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy    281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy    301 MetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy    321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 4
PCT-US00-26524B-2115
; Sequence 2115, Application PC/TUS0026524B
; GENERAL INFORMATION:
;  APPLICANT: Birse et. al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
;  FILE REFERENCE: PA005PCT
;  CURRENT APPLICATION NUMBER: PCT/US00/26524B
;  CURRENT FILING DATE:  2000-09-28
;  PRIOR APPLICATION NUMBER: 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: 60/163,280
;  PRIOR FILING DATE: 1999-11-03
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;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2115
;   LENGTH: 1877
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US00-26524B-2115

Alignment Scores:
Pred. No.:              7.89e-191       Length:         1877
Score:                  2136.00         Matches:        413
Percent Similarity:     99.52%          Conservative:   0
Best Local Similarity:  99.52%          Mismatches:     2
Query Match:            99.30%          Indels:         0
DB:                     1               Gaps:           0

US-09-101-518A-2 (1-415) x PCT-US00-26524B-2115 (1-1877)

Qy      1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy     21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy     41 ThrAlaProSerSerProProheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy     61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy     81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
          |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 AGTGAMTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy    101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
          |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db    473 GCCTTCCTGCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy    121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy    141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 CACCTAGCTGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy    161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy    181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy    201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy    221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy    261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy    281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy    301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy    321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 5
US-60-258-273-3/c
; Sequence 3, Application US/60258273
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
;  TITLE OF INVENTION:  HORMONE RECEPTOR PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001042-PROV
;  CURRENT APPLICATION NUMBER: US/60/258,273
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 6604
;   TYPE: DNA
;   ORGANISM: Human
US-60-258-273-3

Alignment Scores:
Pred. No.:              3.07e-188       Length:         6604
Score:                  2116.00         Matches:        414
Percent Similarity:     99.28%          Conservative:   0
Best Local Similarity:  99.28%          Mismatches:     1
Query Match:            98.37%          Indels:         2
DB:                     64              Gaps:           0

US-09-101-518A-2 (1-415) x US-60-258-273-3 (1-6604)

Qy      1 MetGluLeuArgLysTyrGly-ProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAl 20
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   3700 ATGGAGTTGAGGAAGTACGGTCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGC 3641

Qy     20 aGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTy 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3640 TCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTA 3581

Qy     40 rThrAlaProSerSerProProheProProSerGlnValSerAspHisGlnValLeuAsnAs 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3580 CACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGA 3521

Qy     60 pAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGl 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3520 CGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGA 3461
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Qy      80 uSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspAr 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3460 GAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCG 3401

Qy     100 gAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAl 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3400 GGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGC 3341

Qy     120 aValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLe 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3340 GGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCT 3281

Qy     140 uHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAl 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3280 CCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGC 3221

Qy     160 aAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIl 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3220 TGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACAT 3161

Qy     180 eAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIl 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3160 CAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACAT 3101

Qy     200 eValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLe 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3100 AGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCT 3041

Qy     220 uAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHi 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3040 GGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCA 2981

Qy     240 sHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGlnValGlyArgTh 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2980 CCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCAC 2921

Qy     260 rAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTy 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2920 GGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTA 2861

Qy     280 rCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAl 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2860 CTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGC 2801

Qy     300 aMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLe 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2800 CATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCT 2741

Qy     320 uValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGl 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2740 GGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGA 2681

Qy     340 uSerArgVal-AspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysL 360
           |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2680 AAGCAGGGTAGTACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCC 2621

Qy     360 euAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuL 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2620 TCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGC 2561

Qy     380 euLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgA 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2560 TCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCC 2501

Qy     400 rgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    2500 GGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 2454

RESULT 6
US-09-016-434-1052
; Sequence 1052, Application US/09016434
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1052:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1293 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1002740
US-09-016-434-1052

Alignment Scores:
Pred. No.:                4.33e-185       Length:          1293
Score:                    2073.00         Matches:         400
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              96.37%          Indels:          0
DB:                       14              Gaps:            0

US-09-101-518A-2 (1-415) x US-09-016-434-1052 (1-1293)

Qy      16 IleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPhe 35
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy      36 LeuProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy      56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAsp 75
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy      76 TyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy      96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300
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Qy    116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy    136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy    156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy    176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy    196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy    216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy    236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy    256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

RESULT 7
US-09-960-706-962
; Sequence 962, Application US/09960706
; GENERAL INFORMATION:
;  APPLICANT: Munger, William E.
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
;  TITLE OF INVENTION: Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-01US
;  CURRENT APPLICATION NUMBER: US/09/960,706
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/223,323
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 09/873,319
;  PRIOR FILING DATE: 2001-06-05
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
;   LENGTH: 1293
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U32674
US-09-960-706-962

Alignment Scores:
Pred. No.:                4.33e-185      Length:          1293
Score:                    2073.00        Matches:         400
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              96.37%         Indels:          0
DB:                       36             Gaps:            0

US-09-101-518A-2 (1-415) x US-09-960-706-962 (1-1293)

Qy     16 IleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPhe 35
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy     36 LeuProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy     56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAsp 75
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy     76 TyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy     96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy    116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy    136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy    156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy    176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy    196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy    216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy    236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPhePro 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy    256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780
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Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

RESULT 8
US-09-023-655-980
; Sequence 980, Application US/09023655
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  980:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1552845
US-09-023-655-980

Alignment Scores:
Pred. No.:              2.47e-168      Length:          1670
Score:                  1897.00        Matches:         369
Percent Similarity:     97.63%         Conservative:    1
Best Local Similarity:  97.36%         Mismatches:      5
Query Match:            88.19%         Indels:          4
DB:                     14             Gaps:            1

US-09-101-518A-2 (1-415) x US-09-023-655-980 (1-1670)

Qy     41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
          |||  ||||||           ||||||           :::|||||||||||||||
Db     36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy    317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935
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Qy    337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy    357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy    377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy    397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 9
US-09-624-594-1
; Sequence 1, Application US/09624594
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/624,594
;      FILING DATE:  25-JUL-2000
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/709,838
;      FILING DATE:  10-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  69..1172
US-09-624-594-1

Alignment Scores:
Pred. No.:              2.47e-168      Length:          1670
Score:                  1897.00        Matches:         369
Percent Similarity:     97.63%         Conservative:    1
Best Local Similarity:  97.36%         Mismatches:      5
Query Match:            88.19%         Indels:          4
DB:                     24             Gaps:            1

US-09-101-518A-2 (1-415) x US-09-624-594-1 (1-1670)

Qy     41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
          |||   ||||||            ||||||           :::|||||||||||||||||
```

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Db     36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy    317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy    337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy    357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy    377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy    397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172
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RESULT 10
US-09-633-541-1
; Sequence 1, Application US/09633541
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/633,541
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/709,838
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  69..1172
US-09-633-541-1

Alignment Scores:
Pred. No.:              2.47e-168      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     24             Gaps:           1

US-09-101-518A-2 (1-415) x US-09-633-541-1 (1-1670)

Qy      41 ThrAlaProSer----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||          ||||||          :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 11
US-09-663-702-1
; Sequence 1, Application US/09663702
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;                   Qin, Shixin
;                   Mackay, Charles R.
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
```

```
;              STREET: Two Militia Drive
;              CITY: Lexington
;              STATE: MA
;              COUNTRY: USA
;              ZIP: 02173
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/663,702
;              FILING DATE: 15-Sep-2000
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/829,839
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Brook Esq., David E.
;              REGISTRATION NUMBER: 22,592
;              REFERENCE/DOCKET NUMBER: TKI96-01A
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (617) 861-6240
;              TELEFAX: (617) 861-9540
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1670 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: unknown
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION:  69..1172
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-702-1

Alignment Scores:
Pred. No.:                2.47e-168       Length:          1670
Score:                    1897.00         Matches:         369
Percent Similarity:       97.63%          Conservative:    1
Best Local Similarity:    97.36%          Mismatches:      5
Query Match:              88.19%          Indels:          4
DB:                       26              Gaps:            1

US-09-101-518A-2 (1-415) x US-09-663-702-1 (1-1670)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||           ||||||           :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 12
US-09-663-799-1
; Sequence 1, Application US/09663799
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,799
;             FILING DATE: 15-Sep-2000
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;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/709,838
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1670 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  69..1172
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-799-1

Alignment Scores:
Pred. No.:              2.47e-168      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     26             Gaps:           1

US-09-101-518A-2 (1-415) x US-09-663-799-1 (1-1670)

Qy      41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||            ||||||           :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635
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Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 13
US-09-880-107-3833
; Sequence 3833, Application US/09880107
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3833
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. X95876
US-09-880-107-3833

Alignment Scores:
Pred. No.:              2.47e-168      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     33             Gaps:           1

US-09-101-518A-2 (1-415) x US-09-880-107-3833 (1-1670)

Qy      41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
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Db     36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76

Db     96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96

Db    156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116

Db    216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136

Db    276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156

Db    336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176

Db    396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196

Db    456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216

Db    516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236

Db    576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256

Db    636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276

Db    696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296

Db    756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316

Db    816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy    317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336

Db    876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy    337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356

Db    936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy    357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376

Db    996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy    377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396

Db   1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy    397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415

Db   1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172
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RESULT 14
US-09-170-496-19
; Sequence 19, Application US/09170496
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496-19

Alignment Scores:

Pred. No.:	5.36e-168	Length:	1107
Score:	1891.00	Matches:	364
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.73%	Mismatches:	0
Query Match:	87.91%	Indels:	0
DB:	15	Gaps:	0

US-09-101-518A-2 (1-415) x US-09-170-496-19 (1-1107)

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Db     10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90

Db     70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110

Db    130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130

Db    190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150

Db    250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170

Db    310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190

Db    370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210

Db    430 TGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGG 489

Qy    211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230

Db    490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250

Db    550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy    251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
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Db    610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy    271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729

Qy    291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy    311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy    331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACC 909

Qy    351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy    371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
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Db    970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029

Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
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Db   1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089

Qy    411 SerTyrSerGlyLeu 415
          |||||||||||||||
Db   1090 TCCTACTCGGGCTTG 1104

RESULT 15
US-09-170-496C-19
; Sequence 19, Application US/09170496C
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496C
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-170-496C-19

Alignment Scores:
Pred. No.:              5.36e-168       Length:         1107
Score:                  1891.00         Matches:        364
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.73%          Mismatches:     0
Query Match:            87.91%          Indels:         0
DB:                     15              Gaps:           0

US-09-101-518A-2 (1-415) x US-09-170-496C-19 (1-1107)

Qy     51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
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Db     10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
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Db     70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
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Db    130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
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Db    190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
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Db    250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
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Db    490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
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Db    550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy    251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
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Db    610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy    271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
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Db    670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729

Qy    291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy    311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
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Db    790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy    331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
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Db    910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy    371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
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Db    970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029

Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089

Qy    411 SerTyrSerGlyLeu 415
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Db   1090 TCCTACTCGGGCTTG 1104


Search completed: November  2, 2002, 13:15:40
Job time : 2919 secs
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GenCore version 5.1.3

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 2, 2002, 12:15:06 ; Search time 387 Seconds
(without alignments)
3874.765 Million cell updates/sec

Title: US-09-101-518A-2
Perfect score: 2151
Sequence: 1 MELRKYGPGRLAGTVIGGAA.....SSSRRDSSWSETSEASYSGL 415

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2893907 seqs, 1806667767 residues

Total number of hits satisfying chosen parameters: 5787814

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09101518_@CGN_1_1_200_@runat_29102002_091057_29944
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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15: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2151	100.0	1876	9	US-09-101-518A-1	Sequence 1, Appli
2	2136	99.3	1877	12	US-10-106-698-2125	Sequence 2125, Ap
3	2073	96.4	1293	2	PCT-US02-30182-962	Sequence 962, App
4	1897	88.2	1670	2	PCT-US02-18947-620	Sequence 620, App
5	1897	88.2	1670	2	PCT-US02-25766-2790	Sequence 2790, Ap
6	1897	88.2	1670	12	US-10-172-118-620	Sequence 620, App
7	1897	88.2	1670	13	US-10-251-686-1	Sequence 1, Appli
8	1891	87.9	1107	11	US-10-251-385-19	Sequence 19, Appl
9	1885	87.6	1107	11	US-10-251-385-173	Sequence 173, App
10	648	30.1	34570	13	US-10-035-832-1409	Sequence 1409, Ap
11	640	29.8	1125	13	US-10-035-832-1411	Sequence 1411, Ap
12	640	29.8	2517	13	US-10-035-832-1410	Sequence 1410, Ap
13	637.5	29.6	1777	13	US-10-252-157-227	Sequence 227, App
14	635	29.5	1119	11	US-10-251-385-65	Sequence 65, Appl
15	635	29.5	1119	13	US-10-035-832-1414	Sequence 1414, Ap
16	635	29.5	2818	9	US-09-442-384B-424	Sequence 424, App
17	635	29.5	2824	13	US-10-035-832-1413	Sequence 1413, Ap
18	633	29.4	1119	11	US-10-251-385-199	Sequence 199, App
19	632.5	29.4	32404	13	US-10-035-832-1412	Sequence 1412, Ap
20	610	28.4	2062	12	US-10-143-982-14	Sequence 14, Appl
21	609	28.3	1933	9	US-09-053-375B-415	Sequence 415, App
22	609	28.3	1933	9	US-09-442-384B-420	Sequence 420, App
23	606.5	28.2	1053	2	PCT-US02-15638-2	Sequence 2, Appli
24	603.5	28.1	4452	2	PCT-US02-15638-1	Sequence 1, Appli
25	602	28.0	1440	12	US-10-143-982-110	Sequence 110, App
26	602	28.0	1440	13	US-10-211-364-127	Sequence 127, App
27	602	28.0	1440	13	US-10-212-054-109	Sequence 109, App
28	602	28.0	1440	13	US-10-213-073-54	Sequence 54, Appl
29	602	28.0	1440	13	US-10-216-428-31	Sequence 31, Appl
30	602	28.0	1440	13	US-10-216-436-83	Sequence 83, Appl
31	602	28.0	1440	13	US-10-216-893-38	Sequence 38, Appl
32	602	28.0	1440	13	US-10-219-917-45	Sequence 45, Appl
33	589.5	27.4	31670	13	US-10-035-832-974	Sequence 974, App
34	588	27.3	2139	2	PCT-US02-18947-678	Sequence 678, App
35	588	27.3	2139	12	US-10-172-118-678	Sequence 678, App
36	588	27.3	2139	13	US-10-035-832-975	Sequence 975, App
37	588	27.3	2172	13	US-10-247-671-43	Sequence 43, Appl
38	588	27.3	2192	12	US-10-143-982-64	Sequence 64, Appl
39	586	27.2	1137	11	US-10-251-385-73	Sequence 73, Appl
40	586	27.2	1137	13	US-10-035-832-976	Sequence 976, App
41	584	27.2	1137	11	US-10-251-385-203	Sequence 203, App
42	584	27.2	1758	9	US-09-646-785A-4	Sequence 4, Appli
43	584	27.2	1877	9	US-09-053-375B-727	Sequence 727, App
44	579.5	26.9	5161	12	US-10-160-401-1	Sequence 1, Appli
45	578.5	26.9	1670	2	PCT-US02-25766-3359	Sequence 3359, Ap

ALIGNMENTS

RESULT 1
US-09-101-518A-1
; Sequence 1, Application US/09101518A
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
; FILE REFERENCE: PF218US
; CURRENT APPLICATION NUMBER: US/09/101,518A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: PCT/US96/00499
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)..(1420)
; OTHER INFORMATION:
US-09-101-518A-1

Alignment Scores:
Pred. No.: 1.82e-190 Length: 1876
Score: 2151.00 Matches: 415
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity:  100.00%       Mismatches:    0
Query Match:            100.00%       Indels:        0
DB:                     9             Gaps:          0

US-09-101-518A-2 (1-415) x US-09-101-518A-1 (1-1876)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 AGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     473 GCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532

Qy     121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy     141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     593 CACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy     161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy     181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy     201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy     221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy     241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGlnValGlyArgThr 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy     261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy     281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy     301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy     321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy     341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy     361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy     381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy     401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||
Db    1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 2
US-10-106-698-2125
; Sequence 2125, Application US/10106698
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2125
;   LENGTH: 1877
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-106-698-2125

Alignment Scores:
Pred. No.:              4.53e-189     Length:        1877
Score:                  2136.00       Matches:       413
Percent Similarity:     99.52%        Conservative:  0
Best Local Similarity:  99.52%        Mismatches:    2
Query Match:            99.30%        Indels:        0
DB:                     12            Gaps:          0

US-09-101-518A-2 (1-415) x US-10-106-698-2125 (1-1877)

Qy       1 MetGluLeuArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAla 20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 ATGGAGTTGAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCT 232

Qy      21 GlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyr 40
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTAC 292

Qy      41 ThrAlaProSerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAsp 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     293 ACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGAC 352

Qy      61 AlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGlu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     353 GCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAG 412

Qy      81 SerAspSerCysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArg 100
           |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     413 AGTGAMTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGG 472

Qy     101 AlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAla 120
           ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
Db     473 GCCTTCCTGCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCG 532
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Qy    121 ValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeu 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 GTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTC 592

Qy    141 HisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAla 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 CACCTAGCTGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCT 652

Qy    161 AlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIle 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 GCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATC 712

Qy    181 AsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIle 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 AACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATA 772

Qy    201 ValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeu 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 GTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTG 832

Qy    221 AlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHis 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    833 GCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCAC 892

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProProGlnValGlyArgThr 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 CACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACG 952

Qy    261 AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyr 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 GCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTAC 1012

Qy    281 CysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArgArgLeuArgAla 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 TGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCC 1072

Qy    301 MetArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeu 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 ATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTG 1132

Qy    321 ValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGlu 340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 GTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAA 1192

Qy    341 SerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeu 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 AGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTC 1252

Qy    361 AsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeu 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 AACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTC 1312

Qy    381 LeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArg 400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGG 1372

Qy    401 AspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417

RESULT 3
PCT-US02-30182-962
; Sequence 962, Application PC/TUS0230182
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  APPLICANT:  Munger, William E.
;  APPLICANT:  Kulkarni, Prakash
;  APPLICANT:  Getzenberg, Robert H.
;  APPLICANT:  Waga, Iwao
;  APPLICANT:  Yamamoto, Jun
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
;  TITLE OF INVENTION:  Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-01-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/30182
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: 09/960,706
;  PRIOR FILING DATE: 2001-09-24
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
;   LENGTH: 1293
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U32674
PCT-US02-30182-962

Alignment Scores:
Pred. No.:              2.08e-183       Length:         1293
Score:                  2073.00         Matches:        400
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            96.37%          Indels:         0
DB:                     2               Gaps:           0

US-09-101-518A-2 (1-415) x PCT-US02-30182-962 (1-1293)

Qy     16 IleGlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPhe 35
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy     36 LeuProGlyLeuTyrThrAlaProSerSerProPheProProSerGlnValSerAspHis 55
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy     56 GlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAsp 75
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy     76 TyrGlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSer 95
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy     96 LeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeu 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy    116 LeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThr 135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy    136 AspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeu 155
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy    156 TrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGly 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy    176 AlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAsp 195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy    196 ArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgVal 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy    216 ThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIle 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy    236 PheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProPro 255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720
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Qy    256 GlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

RESULT 4
PCT-US02-18947-620
; Sequence 620, Application PC/TUS0218947
; GENERAL INFORMATION:
;  APPLICANT: Rosetta Inpharmatics
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-228
;  CURRENT APPLICATION NUMBER: PCT/US02/18947
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 620
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NM_001504
;   DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-620

Alignment Scores:
Pred. No.:              7.04e-167      Length:          1670
Score:                  1897.00        Matches:         369
Percent Similarity:     97.63%         Conservative:    1
Best Local Similarity:  97.36%         Mismatches:      5
Query Match:            88.19%         Indels:          4
DB:                     2              Gaps:            1

US-09-101-518A-2 (1-415) x PCT-US02-18947-620 (1-1670)

Qy     41 ThrAlaProSer------------SerProPheProProSerGlnValSerAspHisGln 56
          |||   ||||||           ||||||           :::|||||||||||||||
Db     36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy     57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy     77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy     97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy    117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy    137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy    157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy    177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy    197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy    217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy    237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy    257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy    297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy    317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy    337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy    357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy    377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy    397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 5
PCT-US02-25766-2790
; Sequence 2790, Application PC/TUS0225766
; GENERAL INFORMATION:
;  APPLICANT: GENE LOGIC, INC.
;  APPLICANT:  MUNGER, William E
;  APPLICANT:  FAULK, Ronald
```

```
;  APPLICANT:  SUN, Hongwei
;  APPLICANT:  SASAI, Hitoshi
;  APPLICANT:  WAGA, Iwao
;  APPLICANT:  YAMAMOTO, Jun
;  TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
;  FILE REFERENCE: 44921-5068-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/25766
;  CURRENT FILING DATE:  2002-08-14
;  PRIOR APPLICATION NUMBER: US 60/311,837
;  PRIOR FILING DATE: 2001-08-14
;  NUMBER OF SEQ ID NOS: 13946
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2790
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. X95876
PCT-US02-25766-2790

Alignment Scores:
Pred. No.:              7.04e-167      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     2              Gaps:           1

US-09-101-518A-2 (1-415) x PCT-US02-25766-2790 (1-1670)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
           |||   ||||||           ||||||           :::|||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 6
US-10-172-118-620
; Sequence 620, Application US/10172118
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Chris
;  APPLICANT:  Van 't Veer, Laura
;  APPLICANT:  Van de Vijver, Marc
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-999
;  CURRENT APPLICATION NUMBER: US/10/172,118
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 620
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NM_001504
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-620

Alignment Scores:
Pred. No.:              7.04e-167      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     12             Gaps:           1

US-09-101-518A-2 (1-415) x US-10-172-118-620 (1-1670)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
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Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215

Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172
```

```
RESULT 7
US-10-251-686-1
; Sequence 1, Application US/10251686
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;                   Qin, Shixin
;                   Mackay, Charles R.
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/251,686
;             FILING DATE: 20-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/829,839
;             FILING DATE: 31-MAR-1997
;             APPLICATION NUMBER: US 08/709,838
;             FILING DATE: 10-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1670 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  69..1172
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-251-686-1

Alignment Scores:
Pred. No.:              7.04e-167      Length:         1670
Score:                  1897.00        Matches:        369
Percent Similarity:     97.63%         Conservative:   1
Best Local Similarity:  97.36%         Mismatches:     5
Query Match:            88.19%         Indels:         4
DB:                     13             Gaps:           1

US-09-101-518A-2 (1-415) x US-10-251-686-1 (1-1670)

Qy      41 ThrAlaProSer-----------SerProPheProProSerGlnValSerAspHisGln 56
              |||   ||||||            ||||||          :::||||||||||||||||
Db      36 ACACCACCCAGCAGCCAGAGCACCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAA 95

Qy      57 ValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyr 76
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      96 GTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTAT 155

Qy      77 GlyGluAsnGluSerAspSerCysCysThrSerProProCysProGlnAspPheSerLeu 96
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     156 GGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTG 215
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Qy      97 AsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeu 116
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     216 AACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTG 275

Qy     117 GlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAsp 136
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 GGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGAC 335

Qy     137 ThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrp 156
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 ACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGG 395

Qy     157 AlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAla 176
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCC 455

Qy     177 LeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArg 196
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     456 CTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGC 515

Qy     197 TyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThr 216
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 TACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACC 575

Qy     217 LeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePhe 236
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTC 635

Qy     237 LeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGln 256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAG 695

Qy     257 ValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 GTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTG 755

Qy     277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGlnArg 296
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     756 GTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGG 815

Qy     297 ArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrpThr 316
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     816 CGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACC 875

Qy     317 ProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsn 336
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     876 CCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAAC 935

Qy     337 CysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMet 356
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     936 TGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATG 995

Qy     357 HisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMet 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     996 CACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATG 1055

Qy     377 TrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSer 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1056 TGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCG 1115

Qy     397 SerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSerTyrSerGlyLeu 415
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1116 TCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1172

RESULT 8
US-10-251-385-19
; Sequence 19, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-251-385-19

Alignment Scores:
Pred. No.:              1.52e-166       Length:         1107
Score:                  1891.00         Matches:        364
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.73%          Mismatches:     0
Query Match:            87.91%          Indels:         0
DB:                     11              Gaps:           0

US-09-101-518A-2 (1-415) x US-10-251-385-19 (1-1107)

Qy      51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
           :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy      71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy      91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy     111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy     131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy     151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy     171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy     191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     430 TGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGG 489

Qy     211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy     231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy     251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy     271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729
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Qy    291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy    311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy    331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACC 909

Qy    351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy    371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029

Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089

Qy    411 SerTyrSerGlyLeu 415
          |||||||||||||||
Db   1090 TCCTACTCGGGCTTG 1104
```

RESULT 9
US-10-251-385-173
; Sequence 173, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-173

Alignment Scores:

Pred. No.:	5.49e-166	Length:	1107
Score:	1885.00	Matches:	363
Percent Similarity:	99.73%	Conservative:	1
Best Local Similarity:	99.45%	Mismatches:	1
Query Match:	87.63%	Indels:	0
DB:	11	Gaps:	0

US-09-101-518A-2 (1-415) x US-10-251-385-173 (1-1107)

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Qy     51 GlnValSerAspHisGlnValLeuAsnAspAlaGluValAlaAlaLeuLeuGluAsnPhe 70
          :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 GAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTC 69

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 AGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGC 129

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 CCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTC 189

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 TTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACA 249

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTG 309

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    310 CTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTC 369

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 TGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCC 429

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 TGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGG 489

Qy    211 ProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPheAla 230
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    490 CCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCC 549

Qy    231 LeuProAspPheIlePheLeuSerAlaHisHisAspGluArgLeuAsnAlaThrHisCys 250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    550 CTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGC 609

Qy    251 GlnTyrAsnPheProGlnValGlyArgThrAlaLeuArgValLeuGlnLeuValAlaGly 270
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    610 CAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGC 669

Qy    271 PheLeuLeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu 290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    670 TTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTG 729

Qy    291 ValSerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAla 310
          |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db    730 GTTTCCAGGGGCCAGCGGCGCCTGCGGGCCAAGCGGCTGGTGGTGGTGGTCGTGGTGGCC 789

Qy    311 PheAlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeu 330
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    790 TTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTG 849

Qy    331 GlyAlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThr 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    850 GGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACC 909

Qy    351 SerGlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyVal 370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    910 TCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTC 969

Qy    371 LysPheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGly 390
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    970 AAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGG 1029

Qy    391 LeuGlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAla 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1030 CTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCC 1089

Qy    411 SerTyrSerGlyLeu 415
          |||||||||||||||
Db   1090 TCCTACTCGGGCTTG 1104

RESULT 10
US-10-035-832-1409
; Sequence 1409, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
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;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1409
;   LENGTH: 34570
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(448)
;   OTHER INFORMATION: "n" at positions 1 thru 448 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6032)..(6550)
;   OTHER INFORMATION: "n" at positions 6032 thru 6550 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (29960)..(29979)
;   OTHER INFORMATION: "n" at positions 29960 thru 29979 can be any base
US-10-035-832-1409

Alignment Scores:
Pred. No.:              6.44e-49        Length:         34570
Score:                  648.00          Matches:        157
Percent Similarity:     52.88%          Conservative:   63
Best Local Similarity:  37.74%          Mismatches:     166
Query Match:            30.13%          Indels:         30
DB:                     13              Gaps:           9

US-09-101-518A-2 (1-415) x US-10-035-832-1409 (1-34570)

Qy      4 ArgLysTyrGlyProGlyArgLeuAlaGlyThrValIleGlyGlyAlaAlaGlnSerLys 23
          :::|||:::   |||||||||      |||   :::   ||||||:::      |||::: 
Db  21978 AAAAAGCATTAGCCTGGAAGG---ACAGGAAACCTCACAGGTGGCAGCTTCCTCTCAGAG 22034

Qy     24 SerGlnThrLysSerAspSerIleThrLysGluPheLeuProGlyLeuTyrThrAlaPro 43
          :::   :::               :::   :::           |||              
Db  22035 GAAAAAAGAAGAAGAAGAAGAAGAAGAAGATAT---------GGCTATCGTTTTCAT 22085

Qy     44 SerSerProPheProProSerGlnValSerAspHisGlnValLeuAsnAspAlaGluVal 63
          |||   |||         |||      :::                             
Db  22086 TTCTCTTTCTTTTGGTCCTTACAGTACAAGGAA-------------------------- 22118

Qy     64 AlaAlaLeuLeuGluAsnPheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSer 83
                |||      :::|||:::|||   :::           :::|||:::       
Db  22119 ---------CTGGCCTTCTACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTC 22169

Qy     84 CysCysThrSerProProCysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeu 103
          |||   |||                                 :::|||         |||::: 
Db  22170 TGCTCTACA---------GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATG 22220

Qy    104 ProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAla 123
          |||      |||||||||:::||||||||||||:::::::||||||      |||       
Db  22221 CCTGTGGCCTACAGCCTCATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTA 22280

Qy    124 ValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAla 143
          :::|||         |||         |||||||||:::|||||||||   |||||||||  
Db  22281 ATCCTGGAGAGGCACCGGCACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCA 22340

Qy    144 ValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGln 163
          |||||||||   |||||||||      ||||||           :::   :::|||      
Db  22341 GTAGCCGACCTTCTCTTAGTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGT 22400

Qy    164 TrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyr 183
          ||||||   |||:::   |||||||||         ||||||      ||||||||||||  
Db  22401 TGGGTCCTAGGGACCTTCCTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTAC 22460

Qy    184 AlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsnIleValHisAla 203
                :::|||||||||||||||||||:::   ||||||||||||   ||||||||||||  
Db  22461 TGCAGCAGCCTGCTGCTGGCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCT 22520

Qy    204 ThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCysLeuAlaValTrp 223
                |||||||||                  :::   :::||||||   |||:::|||  
Db  22521 GTTCACGCCTACCGCCGCCGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGG 22580

Qy    224 GlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAla---------His 240
                      |||||||||||||||:::   :::|||                   |||  
Db  22581 CTGGCCGGCTTCCTGTTCGCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCAT 22640

Qy    241 HisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGlnValGlyArgThr 260
          :::::::::   |||           |||   :::::                 |||  
Db  22641 AACAACGACTCCTTA------CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACT 22694

Qy    261 ------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeu 276
                         |||   |||      :::   |||||||||||||||:::|||  
Db  22695 AGAGCCTGGTTCACCTCCCGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTT 22754

Qy    277 ValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGln 295
          ||||||   :::||||||      ::::::      ||||||         |||       
Db  22755 GTGATGGGATGGTGTTACGTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCT 22814

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValAlaPheAlaLeuCysTrp 315
          :::|||   :::|||:::|||:::   ::::::|||         |||   |||||||||  
Db  22815 CAGCGGCAGAAGGCGGTCAGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGG 22874

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
          :::||||||||||:::|||:::   :::|||   |||       |||   |||:::       
Db  22875 TCGCCCTACCACATTGTCATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGC 22934

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
          :::|||               :::   ||||||   ::::::         ||||||      
Db  22935 AGCTGCGAGCTGAGTGGCTATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTG 22994

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
            |||||||||||||||||:::||||||   |||   |||||||||||||||  
Db  22995 GCACACTGCTGTCTCAATCCCATGCTCTACACCTTCGCTGGCGTAAAGTTCCGCAGTGAC 23054

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
          :::      ||||||   :::||||||||||                |||      |||  
Db  23055 CTCTCTCGGCTTCTGACCAAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTT 23111

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
              :::   |||   ||||||   |||||||:::      |||:::  
Db  23112 TTCCCCAACTGGCGCAAGAGTAGTCTCTCTGAGTCAGAGAATGCTACT 23159

RESULT 11
US-10-035-832-1411
; Sequence 1411, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1411
;   LENGTH: 1125
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-035-832-1411

Alignment Scores:
Pred. No.:              4.79e-50        Length:         1125
Score:                  640.00          Matches:        143
Percent Similarity:     56.29%          Conservative:   54
Best Local Similarity:  40.86%          Mismatches:     139
```

```
Query Match:          29.75%      Indels:       14
DB:                   13          Gaps:          6

US-09-101-518A-2 (1-415) x US-10-035-832-1411 (1-1125)

Qy      70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
           :::|||:::|||   :::          :::|||:::   |||   |||
Db      76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy      90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                      :::|||        |||:::|||      |||||||||
Db     127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186

Qy     110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
           :::|||||||||||||:::::||||||      |||      :::|||          |||
Db     187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy     130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
                 |||||||||:::|||||||||   ||||||||||||||||||   ||||||
Db     247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy     150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
           |||      ||||||          :::   :::|||   ||||||   |||:::
Db     307 GTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy     170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
           |||||||||         ||||||      ||||||||||||      :::||||||:::
Db     367 CTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTCGTG 426

Qy     190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
           |||||||||:::   ||||||||||||   ||||||||||          |||||||||
Db     427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy     210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                     :::   :::||||||   |||:::|||             ||||||
Db     487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy     230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
           |||||||||:::   :::|||                 |||:::::::::   |||
Db     547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

Qy     247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr------------AlaLeu 262
                |||   :::::                  |||
Db     604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy     263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
           |||   |||      :::   |||||||||||||||:::|||||||||   :::||||||
Db     661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy     283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
               ::::::      ||||||         |||      :::|||   :::|||:::
Db     721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy     302 ArgLeuValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
           |||:::   :::::|||         |||   ||||||||||:::||||||||:::|||
Db     781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840

Qy     322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
           :::   :::|||   |||      |||   |||:::      :::|||
Db     841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy     342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
              :::   ||||||   ::::::         ||||||      ||||||||||||||
Db     901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy     362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
           |||:::||||||   |||   ||||||||||||||      :::      ||||||
Db     961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy     382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
           :::||||||||||         |||      |||         :::   |||
Db    1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy     402 SerSerTrpSerGluThrSerGluAlaSer 411
           ||||||   ||||||:::      |||:::
Db    1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107

RESULT 12
US-10-035-832-1410
; Sequence 1410, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1410
;   LENGTH: 2517
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-035-832-1410

Alignment Scores:
Pred. No.:              1.32e-49      Length:          2517
Score:                  640.00        Matches:         143
Percent Similarity:     56.29%        Conservative:    54
Best Local Similarity:  40.86%        Mismatches:      139
Query Match:            29.75%        Indels:          14
DB:                     13            Gaps:            6

US-09-101-518A-2 (1-415) x US-10-035-832-1410 (1-2517)

Qy      70 PheSerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProPro 89
           :::|||:::|||   :::          :::|||:::   |||   |||
Db      76 TACAGTAACAGCACGGAGATTCCCCTACAGGACAGTAACTTCTGCTCTACA--------- 126

Qy      90 CysProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeu 109
                              :::|||        |||:::|||      |||||||||
Db     127 GTCGAGGGACCCTTACTGACGTCCTTTAAGGCGGTATTCATGCCTGTGGCCTACAGCCTC 186

Qy     110 LeuPheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArg 129
           :::|||||||||||||:::::||||||      |||      :::|||          |||
Db     187 ATCTTCCTCCTGGGTATGATGGGAAACATCCTGGTGCTGGTAATCCTGGAGAGGCACCGG 246

Qy     130 ThrAlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeu 149
                 |||||||||:::|||||||||   ||||||||||||||||||   ||||||
Db     247 CACACTCGGAGCTCAACCGAGACCTTCCTGTTCCACCTCGCAGTAGCCGACCTTCTCTTA 306

Qy     150 ValLeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGly 169
           |||      ||||||          :::   :::|||   ||||||   |||:::
Db     307 GTCTTCATCCTGCCTTTTGCAGTGGCTGAGGGCTCTGTGGGTTGGGTCCTAGGGACCTTC 366

Qy     170 LeuCysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeu 189
           |||||||||         ||||||      ||||||||||||      :::||||||:::
Db     367 CTCTGCAAAACTGTGATCGCTCTGCACAAGATCAATTTCTACTGCAGCAGCCTGCTCGTG 426

Qy     190 AlaCysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArg 209
           |||||||||:::   ||||||||||||   ||||||||||          |||||||||
Db     427 GCCTGTATAGCTGTAGACCGGTACCTAGCCATCGTCCATGCTGTTCACGCCTACCGCCGC 486

Qy     210 GlyProProAlaArgValThrLeuThrCysLeuAlaValTrpGlyLeuCysLeuLeuPhe 229
                     :::   :::||||||   |||:::|||             ||||||
Db     487 CGTCGACTCCTCTCCATCCACATCACCTGCACGGCCATTTGGCTGGCCGGCTTCCTGTTC 546

Qy     230 AlaLeuProAspPheIlePheLeuSerAla---------HisHisAspGluArgLeuAsn 246
           |||||||||:::   :::|||                 |||:::::::::   |||
Db     547 GCCTTACCGGAACTCCTCTTTGCCAAGGTTGGCCAACCTCATAACAACGACTCCTTA--- 603

Qy     247 AlaThrHisCysGlnTyrAsnPheProGlnValGlyArgThr------------AlaLeu 262
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```
Db    604 ---CCACAGTGCACCTTCTCCCAGGAAAACGAAGCGGAAACTAGAGCCTGGTTCACCTCC 660

Qy    263 ArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeuLeuValMetAlaTyrCysTyr 282
Db    661 CGTTTCCTCTACCACATCGGGGGCTTCCTACTACCGATGCTTGTGATGGGATGGTGTTAC 720

Qy    283 AlaHisIleLeuAlaValLeuLeu---ValSerArgGlyGlnArgArgLeuArgAlaMet 301
Db    721 GTGGGCGTGGTCCACAGGCTACTGCAGGCCCAGCGGCGCCCTCAGCGGCAGAAGGCGGTC 780

Qy    302 ArgLeuValValValValValValAlaPheAlaLeuCysTrpThrProTyrHisLeuVal 321
Db    781 AGGGTGGCCATTTTAGTGACAAGCATTTTCTTCCTCTGCTGGTCGCCCTACCACATTGTC 840

Qy    322 ValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArgAsnCysGlyArgGluSer 341
Db    841 ATCTTCCTAGATACACTGGAGAGGCTGAAGGCTGTGAATAGCAGCTGCGAGCTGAGTGGC 900

Qy    342 ArgValAspValAlaLysSerValThrSerGlyLeuGlyTyrMetHisCysCysLeuAsn 361
Db    901 TATCTCTCTGTGGCCATCACCTTGTGTGAATTCCTGGGCCTGGCACACTGCTGTCTCAAT 960

Qy    362 ProLeuLeuTyrAlaPheValGlyValLysPheArgGluArgMetTrpMetLeuLeuLeu 381
Db    961 CCCATGCTTTACACCTTCGCTGGCGTAAAGTTCCGCAGTGACCTCTCTCGGCTTCTGACC 1020

Qy    382 ArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnProSerSerSerArgArgAsp 401
Db   1021 AAGCTGGGCTGTGCTGGCCCGGCCTCCCTT---TGCCAACTTTTCCCCAACTGGCGCAAG 1077

Qy    402 SerSerTrpSerGluThrSerGluAlaSer 411
Db   1078 AGTAGTCTCTCTGAGTCAGAGAATGCTACT 1107

RESULT 13
US-10-252-157-227
; Sequence 227, Application US/10252157
; GENERAL INFORMATION:
;  APPLICANT: Faris, Mary
;  APPLICANT:  Pearson, Cecelia I.
;  TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
;  FILE REFERENCE: PA-0027-1 US
;  CURRENT APPLICATION NUMBER: US/10/252,157
;  CURRENT FILING DATE:  2002-10-01
;  PRIOR APPLICATION NUMBER: 60/295,048
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 501
;  SOFTWARE: PERL Program
; SEQ ID NO 227
;   LENGTH: 1777
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 218524.4
US-10-252-157-227

Alignment Scores:
Pred. No.:              1.46e-49      Length:         1777
Score:                  637.50        Matches:        154
Percent Similarity:     51.09%        Conservative:   57
Best Local Similarity:  37.29%        Mismatches:     145
Query Match:            29.64%        Indels:         57
DB:                     13            Gaps:           10

US-09-101-518A-2 (1-415) x US-10-252-157-227 (1-1777)

Qy     17 GlyGlyAlaAlaGlnSerLysSerGlnThrLysSerAspSerIleThrLysGluPheLeu 36
Db    353 GGAGGTGTCCTACAGGTGAAAAGC---------------------------------- 376

Qy     37 ProGlyLeuTyrThrAlaProSerSerProPhePro---ProSerGlnValSerAspHis 55

Db    377 ------------CCAGCGACCCAGTCAGGATTTAAGTTTACCTCAAAAATGGAAGATTTT 424

Qy     56 GlnValLeuAsnAspAlaGluValAlaAlaLeuGluAsnPhe---------------- 70
Db    425 AACATGGAGAGTGACAGC--------------TTTGAAGATTTCTGGAAAGGTGAAGAT 469

Qy     71 SerSerSerTyrAspTyrGlyGluAsnGluSerAspSerCysCysThrSerProProCys 90
Db    470 CTTAGTAATTACAGTTACAGCTCTACCCTGCCCCCTTTTCTACTAGATGCCGCCCCATGT 529

Qy     91 ProGlnAspPheSerLeuAsnPheAspArgAlaPheLeuProAlaLeuTyrSerLeuLeu 110
Db    530 GAACCAGAA---TCCCTGGAAATCAACAAGTATTTTGTGGTCATTATCTATGCCCTGGTA 586

Qy    111 PheLeuLeuGlyLeuLeuGlyAsnGlyAlaValAlaAlaValLeuLeuSerArgArgThr 130
Db    587 TTCCTGCTGAGCCTGCTGGGAAACTCCCTCGTGATGCTGGTCATCTTATACAGCAGGGTC 646

Qy    131 AlaLeuSerSerThrAspThrPheLeuLeuHisLeuAlaValAlaAspThrLeuLeuVal 150
Db    647 GGCCGCTCCGTCACTGATGTCTACCTGCTGAACCTAGCCTTGGCCGACCTACTCTTTGCC 706

Qy    151 LeuThrLeuProLeuTrpAlaValAspAlaAlaValGlnTrpValPheGlySerGlyLeu 170
Db    707 CTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTTTGGCACATTCCTG 766

Qy    171 CysLysValAlaGlyAlaLeuPheAsnIleAsnPheTyrAlaGlyAlaLeuLeuLeuAla 190
Db    767 TGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTATAGTGGCATCCTGCTACTGGCC 826

Qy    191 CysIleSerPheAspArgTyrLeuAsnIleValHisAlaThrGlnLeuTyrArgArgGly 210
Db    827 TGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGC--------------- 871

Qy    211 ProProAlaArgValThrLeuThr--------------------------CysLeuAla 221
Db    872 --------------ACACTGACCCAGAAGCGCTACTTGGTCAAATTCATATGTCTCAGC 916

Qy    222 ValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeuSerAlaHisHis 241
Db    917 ATCTGGGGTCTGTCCTTGCTCCTGGCCCTGCCTGTCTTACTTTTCCGAAGGACCGTCTAC 976

Qy    242 AspGluArgLeuAsnAlaThrHisCysGlnTyrAsnPheProGlnValGly--------- 258
Db    977 TCATCCAATGTTAGCCCAGCC---TGC---------TATGAGGACATGGGCAACAATACA 1024

Qy    259 ---------ArgThrAlaLeuArgValLeuGlnLeuValAlaGlyPheLeuLeuProLeu 275
Db   1025 GCAAACTGGCGGATGCTGTTACGGATCCTGCCCCAGTCCTTTGGCTTCATCGTGCCACTG 1084

Qy    276 LeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeuLeuValSerArgGlyGln 295
Db   1085 CTGATCATGCTGTTCTGCTACGGATTCACCCTGCGTACGCTGTTTAAGGCCCACATGGGG 1144

Qy    296 ArgArgLeuArgAlaMetArgLeuValValValValValValAlaPheAlaLeuCysTrp 315
Db   1145 CAGAAGCACCGGGCCATGCGGGTCATCTTTGCTGTCGTCCTCATCTTCCTGCTTTGCTGG 1204

Qy    316 ThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGlyAlaLeuAlaArg 335
Db   1205 CTGCCCTACAACCTGGTCCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAG 1264

Qy    336 AsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSerGlyLeuGlyTyr 355
Db   1265 ACCTGTGAGCGCCGCAATCACATCGACCGGGCTCTGGATGCCACCGAGATTCTGGGCATC 1324

Qy    356 MetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLysPheArgGluArg 375
Db   1325 CTTCACAGCTGCCTCAACCCCCTCATCTACGCCTTCATTGGCCAGAAGTTTCGCCATGGA 1384

Qy    376 MetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeuGlnArgGlnPro 395
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Db   1385 CTCCTCAAGATTCTAGCTATACATGGCTTGATCAGCAAGGACTCCCTGCCCAAAGACAGC 1444

Qy    396 SerSerSerArgArgAspSerSerTrpSerGluThrSer 408
Db   1445 AGGCCTTCCTTTGTTGGCTCTTCTTCAGGGCACACTTCC 1483

RESULT 14
US-10-251-385-65
; Sequence 65, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-251-385-65

Alignment Scores:
Pred. No.:              1.39e-49      Length:          1119
Score:                  635.00        Matches:         147
Percent Similarity:     54.72%        Conservative:    50
Best Local Similarity:  40.83%        Mismatches:      145
Query Match:            29.52%        Indels:          18
DB:                     11            Gaps:            8

US-09-101-518A-2 (1-415) x US-10-251-385-65 (1-1119)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
Db      31 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 90

Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
Db      91 TCCCTGGTGGAAAATCATCTCTGCCCTGCCACAGAGGGTCCCCTCATGGCCTCCTTCAAG 150

Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
Db     151 GCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTC 210

Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
Db     211 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 270

Qy     140 LeuHisLeuAlaValAlaAspThrLeuLeuValLeuThrLeuProLeuTrpAlaValAsp 159
Db     271 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 330

Qy     160 AlaAlaValGlnTrpValPheGlySerGlyLeuCysLysValAlaGlyAlaLeuPheAsn 179
Db     331 GGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCTGCACAAA 390

Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
Db     391 GTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCC 450

Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
Db     451 ATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGT 510

Qy     220 LeuAlaValTrpGlyLeuCysLeuLeuPheAlaLeuProAspPheIlePheLeu------ 237
Db     511 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 570

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGln 256
Db     571 AGCCAAGGCCATCACAACAACTCCCTG------CCACGTTGCACCTTCTCCCAAGAGAAC 624

Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
Db     625 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 684

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
Db     685 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 744

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
Db     745 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 804

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
Db     805 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 864

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
Db     865 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 924

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
Db     925 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 984

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
Db     985 TTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1044

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
Db    1045 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1101

RESULT 15
US-10-035-832-1414
; Sequence 1414, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1414
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-035-832-1414

Alignment Scores:
Pred. No.:              1.39e-49      Length:          1119
Score:                  635.00        Matches:         147
Percent Similarity:     54.72%        Conservative:    50
Best Local Similarity:  40.83%        Mismatches:      145
Query Match:            29.52%        Indels:          18
DB:                     13            Gaps:            8

US-09-101-518A-2 (1-415) x US-10-035-832-1414 (1-1119)

Qy      67 LeuGluAsnPheSerSerSerTyr---------AspTyrGlyGluAsnGluSerAsp--- 82
Db      31 CTCGAGAACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACC 90
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```
Qy      83 SerCysCysThrSerProProCysProGln---------AspPheSerLeuAsnPheAsp 99
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Qy     100 ArgAlaPheLeuProAlaLeuTyrSerLeuLeuPheLeuLeuGlyLeuLeuGlyAsnGly 119
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Qy     120 AlaValAlaAlaValLeuLeuSerArgArgThrAlaLeuSerSerThrAspThrPheLeu 139
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Db     211 CTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTG 270

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Db     271 TTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAG 330

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Qy     180 IleAsnPheTyrAlaGlyAlaLeuLeuLeuAlaCysIleSerPheAspArgTyrLeuAsn 199
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Qy     200 IleValHisAlaThrGlnLeuTyrArgArgGlyProProAlaArgValThrLeuThrCys 219
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Db     511 GGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGCCAAAGTC 570

Qy     238 ---SerAlaHisHisAspGluArgLeuAsnAlaThrHisCysGlnTyrAsnProGln 256
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Qy     257 ValGlyArgThr------------AlaLeuArgValLeuGlnLeuValAlaGlyPheLeu 272
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Db     625 CAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCTG 684

Qy     273 LeuProLeuLeuValMetAlaTyrCysTyrAlaHisIleLeuAlaValLeu---LeuVal 291
           ||||||:::|||||||||   :::||||||      ::::::      |||
Db     685 CTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGCC 744

Qy     292 SerArgGlyGlnArgArgLeuArgAlaMetArgLeuValValValValValValAlaPhe 311
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Db     745 CAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTC 804

Qy     312 AlaLeuCysTrpThrProTyrHisLeuValValLeuValAspIleLeuMetAspLeuGly 331
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Db     805 TTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAG 864

Qy     332 AlaLeuAlaArgAsnCysGlyArgGluSerArgValAspValAlaLysSerValThrSer 351
           |||:::         |||              :::   ||||||   ::::::
Db     865 GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG 924

Qy     352 GlyLeuGlyTyrMetHisCysCysLeuAsnProLeuLeuTyrAlaPheValGlyValLys 371
            ||||||      |||||||||||||||||||:::||||||   |||   |||||||||
Db     925 TTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAG 984

Qy     372 PheArgGluArgMetTrpMetLeuLeuLeuArgLeuGlyCysProAsnGlnArgGlyLeu 391
           ||||||      :::      ||||||   :::|||||||||              |||
Db     985 TTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCCCTGCCTCCCTG 1044

Qy     392 GlnArgGlnProSerSerSerArgArgAspSerSerTrpSerGluThrSerGluAlaSer 411
              :::         |||   ||||||   ||||||   ||||||:::      |||:::
Db    1045 TGCCAGCTCTTCCCTAGCTGGCGCAGG---AGCAGTCTCTCTGAGTCAGAGAATGCCACC 1101


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Job time : 431 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 03:19:18 ; Search time 57 Seconds
(without alignments)
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Perfect score: 1876
Sequence: 1 cctgaagggagagcagggag.....atcgtcaggaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1541.6	82.2	1670	3	US-08-709-838-1	Sequence 1, Appli
2	1541.6	82.2	1670	4	US-08-829-839-1	Sequence 1, Appli
3	240	12.8	1679	1	US-08-202-056-6	Sequence 6, Appli
4	240	12.8	1679	1	US-08-076-093A-5	Sequence 5, Appli
5	240	12.8	1679	1	US-08-701-265-5	Sequence 5, Appli
6	240	12.8	1679	2	US-08-284-586-5	Sequence 5, Appli
7	240	12.8	1679	2	US-08-805-478-5	Sequence 5, Appli
8	240	12.8	1679	2	US-08-802-627A-5	Sequence 5, Appli
9	240	12.8	1679	2	US-08-801-238-5	Sequence 5, Appli
10	240	12.8	1679	2	US-08-801-228-5	Sequence 5, Appli
11	240	12.8	1679	3	US-09-104-296-5	Sequence 5, Appli
12	240	12.8	1679	5	PCT-US94-06380-3	Sequence 3, Appli
13	238.4	12.7	2818	3	US-08-982-493-7	Sequence 7, Appli
14	238.4	12.7	2818	4	US-08-628-655-1	Sequence 1, Appli
15	231	12.3	1200	5	PCT-US95-03032-1	Sequence 1, Appli
16	226.2	12.1	1200	5	PCT-US92-02977-1	Sequence 1, Appli
17	217.8	11.6	1373	5	PCT-US92-02977-6	Sequence 6, Appli
18	217.8	11.6	1373	5	PCT-US95-03032-3	Sequence 3, Appli
19	216.6	11.5	1900	1	US-08-153-848-18	Sequence 18, Appl
20	216.6	11.5	1900	3	US-09-299-843A-18	Sequence 18, Appl
21	216.6	11.5	1900	4	US-09-088-337B-18	Sequence 18, Appl
22	216.6	11.5	1900	5	PCT-US93-11153-18	Sequence 18, Appl
23	216.6	11.5	2058	1	US-08-153-848-6	Sequence 6, Appli
24	216.6	11.5	2058	3	US-09-299-843A-6	Sequence 6, Appli
25	216.6	11.5	2058	4	US-09-088-337B-6	Sequence 6, Appli
26	216.6	11.5	2058	5	PCT-US93-11153-6	Sequence 6, Appli
27	216.6	11.5	2160	1	US-08-153-848-14	Sequence 14, Appl
28	216.6	11.5	2160	3	US-09-299-843A-14	Sequence 14, Appl
29	216.6	11.5	2160	4	US-09-088-337B-14	Sequence 14, Appl
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33	211.8	11.3	2154	3	US-08-352-678-1	Sequence 1, Appli
34	211.8	11.3	2154	5	PCT-US93-09636-1	Sequence 1, Appli
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36	203.2	10.8	1748	1	US-08-202-056-8	Sequence 8, Appli
37	198.8	10.6	2085	3	US-09-299-843A-65	Sequence 65, Appl
38	198.8	10.6	2085	4	US-09-088-337B-65	Sequence 65, Appl
39	196.8	10.5	1106	5	PCT-US92-02977-5	Sequence 5, Appli
40	196.8	10.5	1106	5	PCT-US95-03032-4	Sequence 4, Appli
41	196	10.4	2517	3	US-08-982-493-5	Sequence 5, Appli
42	193.6	10.3	2751	1	US-08-153-848-23	Sequence 23, Appl
43	193.6	10.3	2751	3	US-09-299-843A-23	Sequence 23, Appl
44	193.6	10.3	2751	4	US-09-088-337B-23	Sequence 23, Appl
45	193.6	10.3	2751	5	PCT-US93-11153-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-709-838-1
; Sequence 1, Application US/08709838
; Patent No. 6140064
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TKI96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..1172
US-08-709-838-1

Query Match 82.2%; Score 1541.6; DB 3; Length 1670;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Qy    1863 AGGA 1866
           ||||
Db    1618 AGGA 1621


RESULT 2
US-08-829-839-1
; Sequence 1, Application US/08829839
; Patent No. 6184358
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    APPLICANT:  Qin, Shixin
;    APPLICANT:  Mackay, Charles R.
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/829,839
;      FILING DATE:  31-MAR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/709,838
;      FILING DATE:  10-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook Esq., David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  TKI96-01A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  69..1172
US-08-829-839-1

  Query Match             82.2%;  Score 1541.6;  DB 4;  Length 1670;
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  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

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Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
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Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
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Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
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Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
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Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGA 1866
           ||||
Db    1618 AGGA 1621


RESULT 3
US-08-202-056-6
; Sequence 6, Application US/08202056
; Patent No. 5440021
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Lee, James
;    TITLE OF INVENTION:  Antibodies to Human IL-8 Type B Receptor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/202,056
;      FILING DATE:  25-FEB-1994
;      CLASSIFICATION:  436
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-202-056-6

  Query Match             12.8%;  Score 240;  DB 1;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy     463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
           |||| |    |  ||| |||| |    |||||||||| |||| || ||||  || | ||
Db     512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy     523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
           ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db     572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy     583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
           ||||||| |||||||  || || || |||   ||||||||  | |   ||||  |    |
Db     632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy     643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
           |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db     692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy     703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
             |||  ||||||||||    |   ||| || ||||||||||||  | | ||||||||
Db     752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy     763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
           ||||  ||| || || |||  |||   ||||||||   | | ||    |  | |   | |
Db     812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy     823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
           ||||||   | |  |||||  | |  || | ||  | ||| | |||||  |  |||||
Db     872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy     883 GTCGGCCCACCACGACGAGCGCCTCAACGC-----------CACCCACTGCCAATACAA 930
             | |  ||| | | | | |  |||| |            ||||  || |||| | ||
Db     932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy     931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
           |    || |   |   | | |      |    ||  | ||  | |  ||||| || || ||
Db     992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy     988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
           ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db    1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy    1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
             || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db    1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy    1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
             |||||||||| | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db    1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy    1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
             ||  ||| |   | |||    |   |  ||   |  ||||||||   |  |
Db    1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy    1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
             |||||||     ||||||||||||||||  |||||||  | || |  || || ||
Db    1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy    1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
           ||||||       ||| |  ||| ||   |   |||||||  ||  ||
Db    1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 4
US-08-076-093A-5
; Sequence 5, Application US/08076093A
; Patent No. 5543503
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-076-093A-5

  Query Match             12.8%;  Score 240;  DB 1;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy     463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
           |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db     512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy     523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
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Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642

Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930

Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

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Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

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Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 5
US-08-701-265-5
; Sequence 5, Application US/08701265
; Patent No. 5776457
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/701,265
;      FILING DATE:  22-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-701-265-5

  Query Match             12.8%;  Score 240;  DB 1;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642

Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930

Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

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Qy     988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
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Db    1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy    1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
             || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db    1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy    1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
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Db    1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy    1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
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Db    1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy    1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
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Db    1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy    1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
           ||||||       ||| |  ||| ||   |   ||||||||  ||  ||
Db    1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 6
US-08-284-586-5
; Sequence 5, Application US/08284586
; Patent No. 5840856
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/284,586
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/076,093A
;      FILING DATE:  11-Jun-1993
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/677211
;      FILING DATE:  29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 nucleotides
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-284-586-5

  Query Match             12.8%;  Score 240;  DB 2;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy     463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
           |||| |    |  ||| |||| |    ||||||||| |||| || |||||  || | ||
Db     512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy     523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
           ||||| |  ||||    |   | ||| | | |  |||    | |  ||   ||| || ||
Db     572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy     583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
           ||||||| ||||||| || || || |||   |||||||  | |   |||| |    |
Db     632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy     643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
           |  || |   | ||   |||||| | ||  |   ||||||||||   |    ||||||
Db     692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy     703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
           |||  ||||||||||     |   ||| || ||||||||||||  | | ||||||||
Db     752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy     763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
           ||||  ||| || || |||  |||   ||||||||   | | ||    |  | |   | |
Db     812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy     823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
           ||||||   | |  ||||  | |  || | ||  | ||| | ||||  |  ||||
Db     872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy     883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
             | |  ||| | | | |  |||| |            |||| || |||| | ||
Db     932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy     931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
           |    || |   |   | | |     |    ||  | ||  | |  ||||| || || ||
Db     992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy     988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
           ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db    1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy    1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
             || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db    1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy    1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
           |||||||||| | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db    1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy    1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
             ||  ||| |   | |||    |   |  ||    |   ||||||||   |  |
Db    1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy    1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
           |||||||      |||||||||||||||||  |||||||  | ||  |  || || ||
Db    1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy    1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
           ||||||       ||| |  ||| ||   |   ||||||||  ||  ||
Db    1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 7
US-08-805-478-5
; Sequence 5, Application US/08805478
; Patent No. 5874543
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Lee, James
;    APPLICANT:  Hebert, Caroline
;    APPLICANT:  Jin Kim, K.
;    TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/805,478
;      FILING DATE:  25-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-805-478-5

  Query Match             12.8%;  Score 240;  DB 2;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 8
US-08-802-627A-5
; Sequence 5, Application US/08802627A
; Patent No. 5892017
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  NUCLEIC ACID ENCODING PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,627A
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
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;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-802-627A-5

  Query Match            12.8%;  Score 240;  DB 2;  Length 1679;
  Best Local Similarity  57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 9
US-08-801-238-5
; Sequence 5, Application US/08801238
; Patent No. 5919896
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  PF4A RECEPTOR
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,238
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-801-238-5

  Query Match            12.8%;  Score 240;  DB 2;  Length 1679;
  Best Local Similarity  57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
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Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

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Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930

Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

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Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104

Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164

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Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224

Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 10
US-08-801-228-5
; Sequence 5, Application US/08801228
; Patent No. 5922541
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, James
;    APPLICANT:  Wood, William I.
;    TITLE OF INVENTION:  METHODS FOR DETECTION AND AMPLIFICATION OF
;    TITLE OF INVENTION:  PF4A RECEPTOR NUCLEIC ACID
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/801,228
;      FILING DATE:  19-Feb-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/284586
;      FILING DATE:  10-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/810782
;      FILING DATE:  19-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0706P2P1D3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-08-801-228-5

  Query Match             12.8%;  Score 240;  DB 2;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642

Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930

Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111
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Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401
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RESULT 11
US-09-104-296-5
; Sequence 5, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, WIlliam I.
; TITLE OF INVENTION: PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1679 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-104-296-5

Query Match 12.8%; Score 240; DB 3; Length 1679;
Best Local Similarity 57.0%; Pred. No. 2.5e-42;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

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Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401
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RESULT 12
PCT-US94-06380-3
; Sequence 3, Application PC/TUS9406380
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline

```
;    APPLICANT:  K. Jin Kim
;    APPLICANT:  Genentech, Inc.
;    TITLE OF INVENTION:  METHODS FOR TREATING INFLAMMATORY DISRODERS
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/06380
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076093
;      FILING DATE:  11-JUN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  706P2P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1679 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US94-06380-3

  Query Match             12.8%;  Score 240;  DB 5;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.5e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 13
US-08-982-493-7
; Sequence 7, Application US/08982493
; Patent No. 6110695
;  GENERAL INFORMATION:
;    APPLICANT:  Gunn, Michael D
;    APPLICANT:  Williams, Lewis T
;    APPLICANT:  Cyster, Jason G
;    TITLE OF INVENTION:  Modulating B Lymphocyte Chemokine /
;    TITLE OF INVENTION:  Receptor Interactions
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  75 DENISE DRIVE
;      CITY:  HILLSBOROUGH
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94010
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/982,493
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  UCSFT98-026
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 343-4341
;      TELEFAX:  (650) 343-4342
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2818 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  85..1200
US-08-982-493-7

  Query Match             12.7%;  Score 238.4;  DB 3;  Length 2818;
  Best Local Similarity   56.9%;  Pred. No. 6.2e-42;
  Matches  506;  Conservative    0;  Mismatches  366;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    228 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 287

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    288 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 347

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    348 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 407

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    408 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 467

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    468 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 527

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    528 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 587

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    588 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 647

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    648 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 707

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    708 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 767

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db    768 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 827

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db    828 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 887

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db    888 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 947

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db    948 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1007

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1008 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1068 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1117


RESULT 14
US-08-628-655-1
; Sequence 1, Application US/08628655
; Patent No. 6232123
;  GENERAL INFORMATION:
;    APPLICANT:  Lipp, Martin
;    APPLICANT:  Forster, Reinhold
;    APPLICANT:  Emrich, Thomas
;    APPLICANT:  Wolf, Ingrid
;    APPLICANT:  Kremmer, Elisabeth
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES AGAINST
;    TITLE OF INVENTION:  LEUCOCYTE-SPECIFIC G PROTEIN-COUPLED RECEPTORS
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds, LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2811
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/628,655
;      FILING DATE:  13-AUG-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  8484-0011-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-493-4935
;      TELEFAX:  650-493-5556
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2818 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  85...1200
;      OTHER INFORMATION:
US-08-628-655-1

  Query Match             12.7%;  Score 238.4;  DB 4;  Length 2818;
  Best Local Similarity   56.9%;  Pred. No. 6.2e-42;
  Matches  506;  Conservative    0;  Mismatches  366;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    228 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 287

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    288 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 347

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    348 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 407

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    408 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 467

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    468 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 527
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Qy     763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
           ||||  ||| || || |||  |||   ||||||||   | | ||    |  | |   | |
Db     528 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 587

Qy     823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
           ||||||   | |  |||||  | |  || | ||  | ||| | |||||  |  |||||
Db     588 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 647

Qy     883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
             | |  ||| | | | | |  |||| |           ||||  || |||| | ||
Db     648 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 707

Qy     931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
           |    || |   |   | | |     |    ||  | ||  | |  ||||| || || ||
Db     708 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 767

Qy     988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
           ||||||| ||||||| |||| ||  |||||  |      |  ||  |  | ||   | ||
Db     768 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 827

Qy    1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
             || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db     828 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 887

Qy    1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
           |||||||||| | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db     888 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 947

Qy    1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
            ||  ||| |   | |||    |   |  ||     |   ||||||||   |  |
Db     948 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1007

Qy    1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
           |||||||     ||||||||||||||||||  |||||||  | || |  || || ||
Db    1008 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067

Qy    1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
           ||||||       ||| |  ||| ||      ||||||||  ||  ||
Db    1068 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1117


RESULT 15
PCT-US95-03032-1
; Sequence 1, Application PC/TUS9503032
;  GENERAL INFORMATION:
;    APPLICANT:  Repligen Corporation
;    APPLICANT:  the Trustees of Boston University
;    TITLE OF INVENTION:  ANTIBODIES TO INTERLEUKIN-8 RECEPTORS AND
;    TITLE OF INVENTION:  METHODS OF USE
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03032
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/237,937
;      FILING DATE:  02-MAY-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/210,250
;      FILING DATE:  15-MAR-94
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/803,842
;      FILING DATE:  09-DEC-91
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/726,606
;      FILING DATE:  09-JUL-91
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/685,101
;      FILING DATE:  10-APR-91
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fasse, J. Peter
;      REGISTRATION NUMBER:  32,983
;      REFERENCE/DOCKET NUMBER:  04766/015WO1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1200
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US95-03032-1

  Query Match           12.3%;  Score 231;  DB 5;  Length 1200;
  Best Local Similarity  55.5%;  Pred. No. 1.9e-40;
  Matches  491;  Conservative    0;  Mismatches  385;  Indels    9;  Gaps    2;

Qy     446 CAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTT 505
           | ||   ||| || ||   |  ||      |  ||   | | ||||   |||  ||||
Db     213 CTGGTAGTCACCCAGACACTTAACAAATATGTTGTGGTCGTCATCTATGCCCTGGTCTTC 272

Qy     506 CTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCC 565
           |||||| | ||||||||||||  |  ||||      ||  | |||  | | ||||    |
Db     273 CTGCTGAGCCTGCTGGGCAACTCCCTGGTGATGCTGGTCATACTGTACAGCCGGAGCAAC 332

Qy     566 CTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTG 625
           |       |||||||  || ||||||  |||| ||  | || |||  |||  | |  |||
Db     333 CGTTCGGTCACCGACGTCTACCTGCTGAACCTGGCCATGGCCGACCTGCTTTTTGCCCTG 392

Qy     626 ACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGC 685
           ||  ||||  ||||||| ||   |   |       ||| | || ||| |   ||| |||
Db     393 ACCATGCCTATCTGGGCCGTCTCCAAGGAAAAAGGCTGGATTTTCGGCACGCCCCTGTGC 452

Qy     686 AAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGC 745
           || ||||         |     |  ||||||||||   |||  ||| || |||||||||
Db     453 AAGGTGGTCTCGCTTGTGAAGGAAGTCAACTTCTACAGTGGAATCCTGCTCCTGGCCTGC 512

Qy     746 ATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCC 805
           |||||  | ||||||||||||  ||| || ||||| || |          || |  || |
Db     513 ATCAGTGTGGACCGCTACCTGGCCATTGTCCATGCTACTCGCACACTGACCCAGAAGCGC 572

Qy     806 CCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTC 865
           |    |   || |  |||  || ||||   |||||| ||| |  ||| |||| ||||
Db     573 C---ACTTGGTCAAGTTCATATGTCTGGGCATCTGGGCGCTGTCTCTGATTTTGTCCCTG 629

Qy     866 CCAGACTTCATCTTCC------TGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCAC 919
           ||   |||| ||||||      | |   | |   || |     |||     |  |    |
Db     630 CCCTTCTTCCTCTTCCGCCAAGTCTTTTCTCCAAACAATTCCAGCCCGGTCTGCTATGAG 689

Qy     920 TGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCT 979
             ||      ||  | ||  |     | |||| ||  |||||| | |||| |
Db     690 GACCTGGGTCACAACACAGCGAAATGGCGCATGGTGCTGCGGATCCTGCCACACACTTTC 749

Qy     980 GGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG 1039
           |||||  | ||||| ||||||||||||    |  |||||||    || ||||  |  ||||
Db     750 GGCTTCATCCTGCCGCTGCTGGTCATGCTGTTTTGCTATGGGTTCACCCTGCGCACGCTG 809

Qy    1040 CTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTG 1099
             |     ||        || |   |  ||||||||||||  |  |  | |  |||||| |
Db     810 TTCCAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTCGCCGTCGTGCTC 869

Qy    1100 GCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGAC 1159
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Db    870 ATCTTCCTTCTCTGCTGGCTGCCCTACAACCTGGTCCTGCTCGCAGACACCCTCATGAGG 929

Qy   1160 CTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTC 1219

Db    930 ACCCACGTGATCCAGGAGACGTGTCAGCGTCGCAATGACATTGACCGGGCCCTGGACGCC 989

Qy   1220 ACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGG 1279

Db    990 ACCGAGATTCTGGGCTTCCTGCACAGCTGCCTCAACCCCATCATCTACGCCTTCATTGGC 1049

Qy   1280 GTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGC 1324

Db   1050 CAAAACTTTCGCAATGGATTCCTCAAGATGCTTGCGGCCCGCGGC 1094
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Search completed: November 2, 2002, 04:19:48
Job time : 75 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 04:18:27 ; Search time 2405 Seconds
(without alignments)
16323.569 Million cell updates/sec

Title: US-09-101-518A-1
Perfect score: 1876
Sequence: 1 cctgaagggagagcagggag.....atcgtcaggaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	1861.2	99.2	271144	9	HSXDPB	AL590763 Homo sapi
2	1548.4	82.5	1670	9	HSGPCRIN8	X95876 H.sapiens m
3	1541.6	82.2	1670	6	AR117009	AR117009 Sequence
4	1473	78.5	1563	9	HSCKRL2	Z79783 H.sapiens G
5	1293	68.9	1293	9	HSU32674	U32674 Human orpha
6	850.2	45.3	1678	10	AF223642	AF223642 Rattus no
7	846.2	45.1	1608	10	AB003174	AB003174 Mus muscu
8	844.4	45.0	1525	10	AF045146	AF045146 Mus muscu
9	317.4	16.9	319	9	AB032735	AB032735 Homo sapi
10	317.4	16.9	319	9	AB032736	AB032736 Homo sapi
11	240	12.8	1679	6	AR015971	AR015971 Sequence
12	240	12.8	1679	6	AR060749	AR060749 Sequence
13	240	12.8	1679	6	AR070434	AR070434 Sequence
14	240	12.8	1679	6	AR103431	AR103431 Sequence
15	240	12.8	1679	6	I13754	I13754 Sequence 6
16	240	12.8	1679	6	I24456	I24456 Sequence 5
17	240	12.8	2020	9	HSMDCR	X68829 H.sapiens m
c 18	240	12.8	158634	2	AP000909	AP000909 Homo sapi
c 19	240	12.8	165394	2	AP000877	AP000877 Homo sapi
c 20	240	12.8	244847	2	AP002357	AP002357 Homo sapi
21	238.4	12.7	2818	6	AR107999	AR107999 Sequence
22	238.4	12.7	2818	6	AR151870	AR151870 Sequence
23	238.4	12.7	2818	9	HSBLR1A	X68149 Homo sapien
24	231	12.3	1068	4	RABIL8C	M74240 Oryctolagus
25	231	12.3	1232	4	RABIL8REC	M82873 Oryctolagus
26	229	12.2	3011	6	AX281745	AX281745 Sequence
27	218	11.6	1050	10	AF452185	AF452185 Rattus no
28	218	11.6	1050	10	RNU90610	U90610 Rattus norv
29	216.6	11.5	1500	9	HSDNABLR2	X84702 H.sapiens B
30	216.6	11.5	1900	6	AR107241	AR107241 Sequence
31	216.6	11.5	2058	6	AR107232	AR107232 Sequence
32	216.6	11.5	2139	9	HUMEBI1CDN	L31581 Human G pro
33	216.6	11.5	2160	6	AR107239	AR107239 Sequence
34	216.6	11.5	2215	9	HUMEBI103	L31584 Human G pro
c 35	216.6	11.5	133801	9	AC004585	AC004585 Homo sapi
36	216.2	11.5	1206	4	RABIL8RSB	L24445 Oryctolagus
37	215.8	11.5	1744	4	BTU19947	U19947 Bos taurus
c 38	213.4	11.4	106991	2	AC016960	AC016960 Homo sapi
39	211.8	11.3	2154	6	AR003349	AR003349 Sequence
40	211.8	11.3	2154	6	AR008561	AR008561 Sequence
41	211.8	11.3	2154	9	HUMGPCRA	L08176 Human Epste
42	210	11.2	1083	5	AY057095	AY057095 Danio rer
43	209.4	11.2	1044	9	AF172242	AF172242 Eulemur m
44	206.8	11.0	1044	9	AF172214	AF172214 Nasalis l
45	206.2	11.0	1044	9	AF172210	AF172210 Pygathrix

ALIGNMENTS

RESULT 1
HSXDPB/c
LOCUS HSXDPB 271144 bp DNA linear PRI 17-JUN-2001
DEFINITION Homo sapiens chromosome X sequence from 6 PACs 1 BAC and 1 cosmid, region GJB1-DXS559 map Xq13.1, complete sequence.
ACCESSION AL590763 AJ239319
VERSION AL590763.1 GI:13751778
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 271144)
AUTHORS Ramser,J., Heitmann,K., Sudbrak,R., Kosiura,A., Klages,S., Steffens,C., Borzym,K., Kube,M., Lehrack,S., Marquardt,I., Schuelzchen,S., Starke,A., Thompson,C., Hennig,S., Francis,F., Nemeth,A., Monaco,A., Lehrach,H. and Reinhardt,R.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 271144)
AUTHORS MPIMG.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-1999) MPIMG, Abt.Lehrach, Max Planck Institut Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany

```
COMMENT     Bases 1. .5000 overlap with AL590762 (HSXDPA).
FEATURES             Location/Qualifiers
     source          1. .271144
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                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq13.1"
                     /clone="PAC RPCI-3 485K11"
                     /clone="PAC RPCI-1 177K5"
                     /clone="PAC RPCI-1 2J13"
                     /clone="PAC RPCI-3 423F18"
                     /clone="PAC RPCI-1 104C1"
                     /clone="cosmid cosE3"
                     /clone="BAC OX1"
                     /clone="PAC RPCI-1 56F19"
                     /clone_lib="RPCI1,3-5  Human PAC library, originating
                     institute: Roswell Park Cancer Institute, Creator: Pieter
                     de Jong, P. Ioannou"
                     /note="region between markers GJB1-DXS559"
BASE COUNT    71233 a  59391 c  63906 g  76614 t
ORIGIN

  Query Match             99.2%;  Score 1861.2;  DB 9;  Length 271144;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1863;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 159360 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGGCAGAGAGGGCTCTGGGCACTGGAGG 159301

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159300 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 159241

Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 159240 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGGCTGAGCGGATGGAGTT 159181

Qy    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159180 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 159121

Qy    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159120 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 159061

Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
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Db 159060 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 159001

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
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Db 159000 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 158941

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158940 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 158881

Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158880 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 158821

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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Db 158820 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 158761

Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158760 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 158701

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158700 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 158641

Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
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Db 158640 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 158581

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158580 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 158521

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158520 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 158461

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
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Db 158460 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 158401

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
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Db 158400 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 158341

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
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Db 158340 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 158281

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
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Db 158280 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 158221

Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
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Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
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Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 158100 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 158041

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
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Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
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Db 157980 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 157921

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
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Db 157920 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 157861

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
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Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
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Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
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Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
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Db 157680 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 157621

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 157620 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 157561
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Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
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Db 157560 ATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 157501

Qy   1861 TCAGGA 1866
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Db 157500 TCAGGA 157495


RESULT 2
HSGPCRIN8
LOCUS       HSGPCRIN8               1670 bp    mRNA    linear   PRI 16-MAY-1997
DEFINITION  H.sapiens mRNA for G-protein coupled receptor.
ACCESSION   X95876
VERSION     X95876.1  GI:1552845
KEYWORDS    G protein-coupled receptor; interleukin-8 receptor.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1670)
  AUTHORS   Loetscher,M., Gerber,B., Loetscher,P., Jones,S.A., Piali,L.,
            Clark-Lewis,I., Baggiolini,M. and Moser,B.
  TITLE     Chemokine receptor specific for IP10 and mig: structure, function,
            and expression in activated T-lymphocytes
  JOURNAL   J. Exp. Med. 184 (3), 963-969 (1996)
  MEDLINE   97188912
REFERENCE   2  (bases 1 to 1670)
  AUTHORS   Loetscher,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-1996) M. Loetscher, Theodor-Kocher Institute,
            University of Bern, Freiestrasse 1, CH-3012 Bern, SWITZERLAND
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
     CDS             69. .1175
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                     /db_xref="SWISS-PROT:P49682"
                     /translation="MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCP
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                     RRGPPARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVL
                     QLVAGFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVL
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     polyA_signal    1602. .1607
     polyA_site      1623
BASE COUNT      319 a    574 c    436 g    341 t
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  Query Match           82.5%;  Score 1548.4;  DB 9;  Length 1670;
  Best Local Similarity   99.0%;  Pred. No. 3.5e-268;
  Matches 1558;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
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Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
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Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
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Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
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Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
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Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
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Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
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Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

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Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
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Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

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Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
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Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
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Qy   1863 AGGAAAAAAAAAAA 1876
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RESULT 3
AR117009
LOCUS       AR117009               1670 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6140064.
ACCESSION   AR117009
VERSION     AR117009.1  GI:14097915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1670)
  AUTHORS   Loetscher,M. and Moser,B.
  TITLE     Method of detecting or identifying ligands, inhibitors or promoters
            of CXC chemokine receptor 3
  JOURNAL   Patent: US 6140064-A 1 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .1670
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BASE COUNT      272 a    574 c    436 g    388 t
ORIGIN

  Query Match             82.2%;  Score 1541.6;  DB 6;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 5.8e-267;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
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Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
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Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

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Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
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Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

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Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGA 1866
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Db    1618 AGGA 1621


RESULT 4
HSCKRL2
LOCUS       HSCKRL2                 1563 bp    DNA     linear   PRI 26-JUL-1997
DEFINITION  H.sapiens G protein-coupled receptor CKR-L2.
ACCESSION   Z79783
VERSION     Z79783.1  GI:2281709
KEYWORDS    G Protein-coupled Receptor CKR-L2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo:
REFERENCE   1  (bases 1 to 1563)
  AUTHORS   Gutierrez,J., Varona,R., Zaballos,A., Lind,P. and Marquez,G.
  TITLE     unpublished
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1563)
  AUTHORS   Zaballos,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) Angel Zaballos, Research, Pharmacia &
            Upjohn, Antonio Lopez 109, Madrid, 28026, Spain
FEATURES             Location/Qualifiers
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BASE COUNT      272 a    497 c    479 g    315 t
ORIGIN

  Query Match           78.5%;  Score 1473;  DB 9;  Length 1563;
  Best Local Similarity  99.7%;  Pred. No. 1.2e-254;
  Matches 1476;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db     143 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCGGATGGGATCACGCAGAAGAATGCGAG 202

Qy     121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     203 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGGCTGAGCGGATGGAGTT 262

Qy     181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     263 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 322

Qy     241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
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Qy     301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
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Db     383 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 442

Qy     361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
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Db     503 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 562

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Qy     541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     683 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 742

Qy     661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     743 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 802

Qy     721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     803 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 862

Qy     781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     863 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 922

Qy     841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     923 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 982

Qy     901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
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Db     983 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 1042

Qy     961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1043 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1102

Qy    1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1103 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1162

Qy    1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1163 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1222

Qy    1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1223 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1282

Qy    1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1283 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1342

Qy    1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1343 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1402

Qy    1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1403 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1462

Qy    1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1463 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1522

Qy    1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCC 1481
          |||||||||||||||||||||||||||||||||||||||||
Db    1523 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCC 1563


RESULT 5
HSU32674
LOCUS       HSU32674                1293 bp    DNA     linear   PRI 05-JUN-1996
DEFINITION  Human orphan receptor GPR9 (GPR9) gene, partial cds.
ACCESSION   U32674
VERSION     U32674.1  GI:1002740
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1293)
  AUTHORS   Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
            Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
            and Docherty,J.M.
  TITLE     Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
            and GPR14, encoding receptors related to interleukin 8,
            neuropeptide Y, and somatostatin receptors
  JOURNAL   Genomics 29 (2), 335-344 (1995)
  MEDLINE   96115583
REFERENCE   2  (bases 1 to 1293)
  AUTHORS   Marchese,A., Heiber,M., Nguyen,T., Heng,H.H.Q., Saldivia,V.R.,
            Cheng,R., Murphy,P.M., Tsui,L.-C., Shi,X., George,S.R., O'Dowd,B.F.
            and Docherty,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1995) B.F. O'Dowd, Department of Pharmacology,
            University of Toronto, 8 Taddle Creek Rd., Toronto, Ontario M5S
            1A8, Canada
FEATURES             Location/Qualifiers
     source          1. .1293
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     gene            1. .1203
                     /gene="GPR9"
     CDS             <109. .1203
                     /gene="GPR9"
                     /note="The initiating methionine has not been found; GPR9
                     is an orphan receptor similar to the interleukin 8
                     receptors"
                     /codon_start=1
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                     /db_xref="GI:1002741"
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                     LNFDRAFLPALYSLLFLLGLLGNGAVAAVLLSRRTALSSTDTFLLHLAVADTLLVLTL
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                     PARVTLTCLAVWGLCLLFALPDFIFLSAHHDERLNATHCQYNFPQVGRTALRVLQLVA
                     GFLLPLLVMAYCYAHILAVLLVSRGQRRLRAMRLVVVVVVAFALCWTPYHLVVLVDIL
                     MDLGALARNCGRESRVDVAKSVTSGLGYMHCCLNPLLYAFVGVKFRERMWMLLLRLGC
                     PNQRGLQRQPSSSRRDSSWSETSEASYSGL"
BASE COUNT      201 a    458 c    357 g    277 t
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 2.5e-222;
  Matches 1293;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     218 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy     278 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy     338 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy     398 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 457
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Db     181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy     458 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy     518 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 577
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Db     301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy     578 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 637
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Db     361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy     638 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy     698 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 757
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Db     481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy     758 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy     818 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy     878 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 937
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Db     661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy     938 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy     998 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 1057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy    1058 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 1117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy    1118 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 1177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy    1178 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy    1238 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1297
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Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy   1298 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy   1358 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

Qy   1418 TGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTC 1477
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Db   1201 TGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTC 1260

Qy   1478 CTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAA 1510
          ||||||||||||||||||||||||||||||||
Db   1261 CTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAA 1293


RESULT 6
AF223642
LOCUS       AF223642 .               1678 bp    mRNA    linear   ROD 19-JUN-2000
DEFINITION  Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds.
ACCESSION   AF223642
VERSION     AF223642.1  GI:8572056
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1678)
  AUTHORS   Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S.
            and Sarau,H.M.
  TITLE     Identification and molecular characterization of rat CXCR3:
            receptor expression and interferon-inducible protein-10 binding are
            increased in focal stroke
  JOURNAL   Mol. Pharmacol. 57 (6), 1190-1198 (2000)
  MEDLINE   20286573
   PUBMED   10825390
REFERENCE   2  (bases 1 to 1678)
  AUTHORS   Wang,X., Li,X., Schmidt,D.B., Foley,J.J., Barone,F.C., Ames,R.S.
            and Sarau,H.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-JAN-2000) Cardiovascular Sciences, DuPont
            Pharmaceuticals, Experimental Station E400/3420B, Wilmington, DE
            19880/0400, USA
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     source          1. .1678
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     CDS             149. .1252
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                     /product="chemokine receptor CXCR3"
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                     /translation="MYLEVSERQVLDASDIAFLLENSTSPYDYGENESDFSDSPPCPQ
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                     LVAGFLMPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVVVAFAVCWTPYHLVVLV
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BASE COUNT      370 a    486 c    417 g    405 t
ORIGIN

  Query Match           45.3%;  Score 850.2;  DB 10;  Length 1678;
  Best Local Similarity  75.1%;  Pred. No. 7.4e-143;
  Matches 1167;  Conservative    0;  Mismatches  348;  Indels   38;  Gaps    7;

Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
          |||| ||||| |  |||||||||| ||| | | ||  |||||   || ||||| |||  ||
Db    159 AGGTCAGTGAACGTCAAGTGCTAGATGCCTCGGACATTGCCTTTCTTCTGGAAAACAGCA 218

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
            ||| |||| || |||||·||||||| || |||   | || |  ||||||||||||||
Db    219 CATCTCCCTACGATTATGGGGAAAACGAAAGCGAC---TTCTCTGACTCCCCGCCCTGCC 275

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
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Db    276 CACAGGACTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGTCCTCTACAGCCTCCTCT 335

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
          || |||||||||||||| ||||| || || ||||| || ||||| |||||| ||| || |
Db    336 TTTTGCTGGGGCTGCTAGGCAATGGGGCAGTGGCTGCTGTGCTACTGAGCCAGCGCACTG 395

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
          |||||||||||| |||||||||||||||||||| ||||| || ||    |||||||| |
Db    396 CCCTGAGCAGCACAGACACCTTCCTGCTCCACCTGGCTGTGGCCGATGTACTGCTGGTAC 455

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
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Db    456 TAACCCTCCCACTGTGGGCAGTAGATGCTGCTGCCCAGTGGGTTTTCGGCTCTGGTCTCT 515

Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
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Db    516 GCAAAGTGGCAGGTGCCCTGTTCAACATCAACTTCTACGCAGGGGCCTTCCTGCTGGCCT 575

Qy    744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
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Db    576 GTATAAGCTTTGACCGCTACCTGAGCATAGTGCATGCCACCCAGATCTACCGCAGGGACC 635

Qy    804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
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Db    636 CCTGGGTACGTGTAGCCCTCACCTGCATTGTTGTGTGGGGTCTCTGTGTGCTCTTTGCCC 695

Qy    864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
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Db    696 TCCCAGATTTCATCTTCCTGTCAGCCAGCCATGATCAGCGCCTCAATGCCACCCATTGCC 755

Qy    924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
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Db    756 AGTACAACTTCCCACAGGTGGGTCGGACTGCTCTGCGTGTACTGCAGCTAGTGGCTGGTT 815

Qy    984 TTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
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Db    816 TCCTGATGCCCCTTCTAGTCATGGCCTACTGCTATGCCCATATCCTGGCTGTGCTGCTGG 875

Qy   1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
          | ||||| ||||| |||| | || || ||| |||| |||||||||| ||||||||||
Db    876 TCTCCAGAGGCCAGAGGCGCTTTCGAGCTATGAGGCTAGTGGTGGTGGTGGTGGTGGCCT 935

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          | | |||||||||||||||||| |||||||||   || ||||| |||||||| |||||||
Db    996 GAGTTTTGGCCCGCAACTGTGGTCGAGAAAGCCATGTGGACGTAGCCAAGTCAGTCACCT 1055

Qy   1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
          ||||| |||||||||||||||||||||||||||||||| || |||||||||||||||| || | |
Db   1056 CAGGCATGGGCTACATGCACTGCTGCCTCAATCCACTGCTCTATGCCTTTGTGGGAGTGA 1115

Qy   1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
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Db   1116 AGTTCAAAGAACAAATGTGGATGTTGCTCATGCGCCTGGGCCGCTCTGACCAGAGAGGAC 1175

Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
            ||| ||||||| || ||||| ||  | || |||||||||||||||||  | |||||||
Db   1176 CGCAGCGGCAGCCTTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCT 1235

Qy   1404 CCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCC 1463
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Db   1236 CCTACTTGGGCTTGTAATTCAGGAATGC-AACTGGAGCCTGTGCAACCCAAGTCCTAACA 1294

Qy   1464 CGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAATATCCTCGCTCCC 1523
Db   1295 CACTCCAGGCTCTTCTCCTTGTAGTTGGGCTAGCTCTAACTTACCCATAACTTTGCTGCT 1354

Qy   1524 GGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCTCTG 1583
Db   1355 GGGACTCAGTGACAG-CTCAGCATATCCAGGTCTCCTGAGAACCACTCTCAGCTCCAAGG 1413

Qy   1584 AGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCCGAGGTGGCTG 1643
Db   1414 ACAGCAGCACCTTTACTGAGCCATGCCCTGCCTCCGCTGTTTT------AGAACTAGTTG 1467

Qy   1644 CCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGTGCGGG 1703
Db   1468 CCTGGAGCCCCACCACCCTTCTAAATTAGCAGATAGCACTCAGCCATCCCTGTGTGAGAA 1527

Qy   1704 GAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCCTCCAGCT 1763
Db   1528 GAGGAAGAGACAAATAGCACTGAAGGCCAGGCCTT----------------------GCT 1565

Qy   1764 CAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTTGGTCTTTTATTTTTATGTC 1823
Db   1566 CAGCACTGAATGTGTTTATGGTCTCCAATATCTCAACATGTGCCC----AATTTTATGGC 1621

Qy   1824 TAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTCAGGAAAAAAAAAAA 1876
Db   1622 TAGAAACCCTGCTTAAAC-TTTCAATAAACAAGATAATGAGGAAAAAAAAAAA 1673


RESULT 7
AB003174
LOCUS       AB003174                1608 bp    mRNA    linear   ROD 28-OCT-1998
DEFINITION  Mus musculus mRNA for interferon-inducible protein 10 receptor,
            complete cds.
ACCESSION   AB003174
VERSION     AB003174.1  GI:3798731
KEYWORDS    interferon-inducible protein 10 receptor.
SOURCE      Mus musculus blood cytotoxic T cells cell_line:CTLL-2 cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1608)
  AUTHORS   Tamaru,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-APR-1997) Masahiro Tamaru, Japan Tobacco Inc. Central
            Pharmaceutical Reseach Institute, Pharmaceutical Frontier Reseach
            Laboratories; 13-2, Fukuura 1-chome, Kanazawa-ku, Yokohama,
            Kanagawa 236, Japan (E-mail:tamaru@ikrl.jti.co.jp,
            Tel:81-45-786-7694, Fax:81-45-786-7692)
REFERENCE   2  (sites)
  AUTHORS   Tamaru,M., Tominaga,Y., Yatsunami,K. and Narumi,S.
  TITLE     Cloning of the murine interferon-inducible protein 10 (IP-10)
            receptor and its specific expression in lymphoid organs
  JOURNAL   Biochem. Biophys. Res. Commun. 251 (1), 41-48 (1998)
  MEDLINE   99009219
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
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                     /cell_type="cytotoxic T cells"
                     /tissue_type="blood"
     gene            90. .1193
                     /gene="MCXCR3"
     CDS             90. .1193
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                     /protein_id="BAA34045.1"
                     /db_xref="GI:3798732"
                     /translation="MYLEVSERQVLDASDFAFLLENSTSPYDYGENESDFSDSPPCPQ
                     DFSLNFDRTFLPALYSLLFLLGLLGNGAVAAVLLSQRTALSSTDTFLLHLAVADVLLV
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                     RDPRVRVALTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQ
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     polyA_site      1608
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ORIGIN

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  Best Local Similarity   76.2%;  Pred. No. 3.9e-142;
  Matches 1095;  Conservative    0;  Mismatches  333;  Indels    9;  Gaps    4;

Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
Db    100 AGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGCA 159

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
Db    160 CCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGCC 216

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
Db    217 CACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTCT 276

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
Db    277 TCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACTG 336

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
Db    337 CCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTGT 396

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
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Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
Db    457 GCAAAGTGGCAGGCGCCTTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTGCTGGCTT 516

Qy    744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
Db    517 GTATAAGCTTCGACAGATATCTGAGCATAGTGCACGCCACCCAGATCTACCGCAGGGACC 576

Qy    804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
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Qy    864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
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Qy    984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
Db    757 TCCTGCTGCCCCTTCTGGTCATGGCCTACTGCTATGCCCATATCCTAGCTGTTCTGCTGG 816

Qy   1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
Db    817 TCTCCAGAGGCCAGAGGCGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTGGCAGCCT 876

Qy   1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
Db    877 TTGCTGTCTGCTGGACCCCCTATCACCTGGTGGTGCTAGTGGATATCCTCATGGATGTGG 936

Qy   1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
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Qy   1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
Db   1057 AGTTCAGAGAGCAAATGTGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAGAGAGGGC 1116

Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
Db   1117 CCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCT 1176

Qy   1404 CCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCGC--CCACAGTCTGACTTC 1461
Db   1177 CCTACCTGGGCTTGTAATTCTGGACTGGAACTGTAGCCTGCGCAGCCCAAGTCCTAACAC 1236

Qy   1462 CCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAATATCCTCGCTC 1521
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Qy   1522 CCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCTC 1581
Db   1297 CCAGGATGCACTGACAGCTCAGCATATATCCAGCTCTCCTG--AGAATCAATCTCAGCAA 1354

Qy   1582 TGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCCGAGG--TG 1639
Db   1355 CAAGGACAACACCATTACTGTGCCTTAGCTGCCATGCCCTATCTTGCTGTTTTAGAACTA 1414

Qy   1640 GCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGTG 1699
Db   1415 GCTGCCTGGAGCCCCACCGCCCTACTAAATTAGCAAGTAGAACTCAGCCATCCCTGTGTG 1474

Qy   1700 CGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCC 1756
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LOCUS       AF045146                1525 bp    mRNA    linear   ROD 10-JUL-1998
DEFINITION  Mus musculus chemokine receptor CXCR3 mRNA, complete cds.
ACCESSION   AF045146
VERSION     AF045146.1  GI:3282809
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1525)
  AUTHORS   Soto,H., Wang,W., Strieter,R.M., Copeland,N.G., Gilbert,D.J.,
            Jenkins,N.A., Hedrick,J. and Zlotnik,A.
  TITLE     The CC chemokine 6Ckine binds the CXC chemokine receptor CXCR3
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (14), 8205-8210 (1998)
  MEDLINE   98318636
REFERENCE   2  (bases 1 to 1525)
  AUTHORS   Soto,H. and Zlotnik,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JAN-1998) Immunobiology, DNAX Research Institute, 901
            California Ave., Palo Alto, CA 94304, USA
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                     /db_xref="GI:3282810"
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                     RDPRVRVALTCIVVWGLCLLFALPDFIYLSANYDQRLNATHCQYNFPQVGRTALRVLQ
                     LVAGFLLPLLVMAYCYAHILAVLLVSRGQRRFRAMRLVVVVVAAFAVCWTPYHLVVLV
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BASE COUNT      316 a    433 c    386 g    390 t
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  Best Local Similarity   76.6%;  Pred. No. 8.2e-142;
  Matches 1101;  Conservative    0;  Mismatches  326;  Indels   11;  Gaps    5;

Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
Db     11 AGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGCA 70

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
Db     71 CCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGCC 127

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
Db    128 CACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTCT 187

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
Db    188 TCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACTG 247

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
Db    248 CCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTGT 307

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
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Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
Db    368 GCAAAGTGGCAGGCGCCTTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTGCTGGCTT 427

Qy    744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
Db    428 GTATAAGCTTCGACAGATATCTGAGCATAGTGCACGCCACCCAGATCTACCGCAGGGACC 487

Qy    804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
Db    488 CCCGGGTACGTGTAGCCCTCACCTGCATAGTTGTATGGGGTCTCTGTCTGCTCTTTGCCC 547

Qy    864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
Db    548 TCCCAGATTTCATCTACCTATCAGCCAACTACGATCAGCGCCTCAATGCCACCCATTGCC 607

Qy    924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
Db    608 AGTACAACTTCCCACAGGTGGGTCGCACTGCTCTGCGTGTACTGCAGCTAGTGGCTGGTT 667

Qy    984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
Db    668 TCCTGCTGCCCCTTCTGGTCATGGCCTACTGCTATGCCCATATCCTAGCTGTTCTGCTGG 727

Qy   1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
Db    728 TCTCCAGAGGCCAGAGGCGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTGGCAGCCT 787

Qy   1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
Db    788 TTGCTGTCTGCTGGACCCCCTATCACCTGGTGGTGCTAGTGGATATCCTCATGGATGTGG 847

Qy   1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
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Qy   1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
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Db    908 CGGGCATGGGGTACATGCACTGCTGCCTCAATCCGCTGCTCTATGCCTTTGTGGGAGTGA 967

Qy   1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
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Db    968 AGTTCAGAGAGAAAATGTGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAGAGAGGGC 1027

Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
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Db   1028 CCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCT 1087

Qy   1404 CCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCGC--CCACAGTCTGACTTC 1461
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Db   1088 CCTACCTGGGCTTGTAATTCTGGACTGGAACTGTAGCCTGCGCAGCCCAAGTCCTAACAC 1147

Qy   1462 CCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAATATCCTCGCTC 1521
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Db   1148 ACTCCAAGTGCTTGTCCTCCTTGTAGTTGGGCTAGCTCGAACTTACCCGTAACTTTGCTG 1207

Qy   1522 CCGGGACTCACTGGCAGC-CCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCT 1580
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Qy   1581 CTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCC--GAGGT 1638
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Db   1265 ACAAGGACAACACCATTACTGTGCCTTAGCTGCCATGCCCTATCTTGCTGTTTTAGAACT 1324

Qy   1639 GGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGT 1698
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Db   1325 AGCTGCCTGGAGCCCCACCGCCCTACTAAATTAGCAAGTAGAACTCAGCCATCCCTGTGT 1384

Qy   1699 GCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCC 1756
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LOCUS       AB032735                319 bp    DNA     linear   PRI 01-DEC-2000
DEFINITION  Homo sapiens gene for chemokine receptor CXCR3, partial cds.
ACCESSION   AB032735
VERSION     AB032735.1  GI:7209692
KEYWORDS    chemokine receptor CXCR3.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Kato,H., Tsuchiya,N. and Tokunaga,K.
  TITLE     Single nucleotide polymorphisms in the coding regions of human
            CXC-chemokine receptors CXCR1, CXCR2 and CXCR3
  JOURNAL   Genes and immunity. 1 (5), 330-337 (2000)
  MEDLINE   21040285
   PUBMED   11196695
REFERENCE   2  (bases 1 to 319)
  AUTHORS   Kato,H., Tsuchiya,N. and Tokunaga,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo,
            Department of Human Genetics, Graduate School of Medicine; 7-3-1
            Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
            (E-mail:katoh@m.u-tokyo.ac.jp, Tel:81-3-5841-3693,
            Fax:81-3-5802-8619)
FEATURES             Location/Qualifiers
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                     /protein_id="BAA92297.1"
                     /db_xref="GI:7209693"
                     /translation="DILMDLGALARNCGQESRVDVAKSVTSGLGYMHCCLNPLLYAFV
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Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
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Db      1 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCAAGAAAGCAGGGTAG 60

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db     61 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 120

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Db    121 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 180

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db    181 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 240

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Db    241 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 300

Qy   1443 TCGCCCACAGTCTGACTTC 1461
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LOCUS       AB032736                319 bp    DNA     linear   PRI 01-DEC-2000
DEFINITION  Homo sapiens gene for chemokine receptor CXCR3, partial cds.
ACCESSION   AB032736
VERSION     AB032736.1  GI:7209694
KEYWORDS    chemokine receptor CXCR3.
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Kato,H., Tsuchiya,N. and Tokunaga,K.
  TITLE     Single nucleotide polymorphisms in the coding regions of human
            CXC-chemokine receptors CXCR1, CXCR2 and CXCR3
  JOURNAL   Genes and immunity. 1 (5), 330-337 (2000)
  MEDLINE   21040285
   PUBMED   11196695
REFERENCE   2  (bases 1 to 319)
  AUTHORS   Kato,H., Tsuchiya,N. and Tokunaga,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1999) Hitoshi Kato, University of Tokyo,
            Department of Human Genetics, Graduate School of Medicine; 7-3-1
            Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
            (E-mail:katoh@m.u-tokyo.ac.jp, Tel:81-3-5841-3693,
            Fax:81-3-5802-8619)
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ORIGIN

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  Best Local Similarity   99.7%;  Pred. No. 3.7e-47;
  Matches  318;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
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Db      1 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 60

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db     61 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 120

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db    181 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 240

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Qy   1443 TCGCCCACAGTCTGACTTC 1461
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Db    301 TCGCCCACAGTCTGACTTC 319


RESULT 11
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LOCUS       AR015971               1679 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 5 from patent US 5776457.
ACCESSION   AR015971
VERSION     AR015971.1  GI:3972248
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Lee,J. and Wood,W.I.
  TITLE     Antibodies to human PF4A receptor and compositions thereof
  JOURNAL   Patent: US 5776457-A 5 07-JUL-1998;
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BASE COUNT      327 a    532 c    457 g    363 t
ORIGIN

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Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
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Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          |||||  |  ||||   |   | |||  | | |  |||    | |  ||  |||  || ||
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          |||||||  |||||||  ||  ||  ||  |||   ||||||||  | |   ||||  |   |
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
          |  ||  |   | ||    ||||||  | ||  |   ||||||||||   |    ||||||
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
          |||  |||||||||||    |   |||  ||  ||||||||||||  | | ||||||||
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  |||  ||  ||  |||  |||   ||||||||   | | ||   |  | |  | |
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||   | |  |||||  | |  || | ||  | ||| | |||||  |  |||||
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
            | |  ||| | | | |  |||| |           ||||  || |||| | ||
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |    |   | | |    |   ||  | ||  | |  |||| || || ||
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          |||||||  |||||||  |||| ||  |||||  |       |  ||  |  | ||   | ||
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
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Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
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Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
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Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
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Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||       ||| |  ||| ||   |   ||||||||  ||  ||
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 12
AR060749
LOCUS       AR060749               1679 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5840856.
ACCESSION   AR060749
VERSION     AR060749.1  GI:5987199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Chuntharapai,A., Lee,J., Hebert,C. and Kim,K.Jin.
  TITLE     Antibodies to a human PF4 superfamily receptor
  JOURNAL   Patent: US 5840856-A 5 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .1679
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                    /organism="unknown"
BASE COUNT      327 a    532 c    457 g    363 t
ORIGIN

  Query Match             12.8%;  Score 240;  DB 6;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.6e-33;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
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Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 13
AR070434
LOCUS       AR070434                1679 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 5 from patent US 5892017.
ACCESSION   AR070434
VERSION     AR070434.1  GI:7221322
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Lee;J. and Wood,W.I.
  TITLE     Nucleic acid encoding PF4A receptor
  JOURNAL   Patent: US 5892017-A 5 06-APR-1999;
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="unknown"
BASE COUNT      327 a    532 c    457 g    363 t
ORIGIN

  Query Match             12.8%;  Score 240;  DB 6;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.6e-33;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
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Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

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Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
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Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

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Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

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Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 14
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LOCUS       AR103431               1679 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6087475.
ACCESSION   AR103431
VERSION     AR103431.1  GI:12815019
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Lee,J. and Wood,W.I.
  TITLE     PF4A receptor
  JOURNAL   Patent: US 6087475-A 5 11-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="unknown"
BASE COUNT      327 a    532 c    457 g    363 t
ORIGIN

  Query Match           12.8%;  Score 240;  DB 6;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.6e-33;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

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Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

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Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

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Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


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LOCUS       I13754                 1679 bp    DNA     linear   PAT 26-SEP-1995
DEFINITION  Sequence 6 from patent US 5440021.
ACCESSION   I13754
VERSION     I13754.1  GI:996820
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Chuntharapai,A., Hebert,C., Kim,K.J. and Lee,J.
  TITLE     Antibodies to human IL-8 type B receptor
  JOURNAL   Patent: US 5440021-A 6 08-AUG-1995;
FEATURES             Location/Qualifiers
     source          1. .1679
                     /organism="unknown"
BASE COUNT      327 a    532 c    457 g    363 t
ORIGIN

  Query Match           12.8%;  Score 240;  DB 6;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 2.6e-33;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

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Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

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Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
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Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104

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Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164

Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224

Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401
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Job time : 2828 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 04:07:46 ; Search time 229 Seconds
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Perfect score: 1876
Sequence: 1 cctgaagggagagcagggag.....atcgtcaggaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1874.4	99.9	1876	18	AAT72800	Human G-protein ch
	2	1873.2	99.9	1877	22	AAH35033	Human colon cancer
	3	1541.6	82.2	1670	19	AAV26557	Human IP-10/Mig re
	4	1097	58.5	1107	21	AAA30593	Human G protein-co
	5	1095.4	58.4	1107	21	AAA30714	DNA encoding human
	6	1094.6	58.3	1159	20	AAZ32713	Human chemokine re
	7	844.4	45.0	1620	19	AAV43793	Rodent chemokine r
	8	240	12.8	1679	13	AAQ37107	New platelet facto
	9	240	12.8	1679	16	AAQ99009	Chemokine superfam
	10	240	12.8	1679	16	AAQ80522	Human lymphocyte P
	11	238.4	12.7	1119	21	AAA30626	Human G protein-co
	12	238.4	12.7	1119	21	AAA30727	DNA encoding human
	13	238.4	12.7	2818	20	AAX87710	Human Burkitt's ly
c	14	238.4	12.7	3620	22	ABA09117	Human Burkitt lymp
	15	231	12.3	1200	13	AAQ30011	Sequence encoding
	16	231	12.3	1200	16	AAQ99949	Recombinant high a
	17	229	12.2	3011	24	AAS94899	Human DNA sequence
	18	229	12.2	4017	23	AAS83768	DNA encoding novel
	19	217.8	11.6	1373	16	AAQ99951	Recombinant high a
	20	216.6	11.5	1137	21	AAA30632	Human G protein-co
	21	216.6	11.5	1710	23	AAS76560	DNA encoding novel
	22	216.6	11.5	1900	15	AAQ66162	Partial coding seq
	23	216.6	11.5	1900	19	AAV18349	Human V31 seven tr
	24	216.6	11.5	1900	21	AAA91709	Human 7TM receptor
	25	216.6	11.5	2058	15	AAQ66153	Putative seven tra
	26	216.6	11.5	2058	19	AAV18345	Human V31 seven tr
	27	216.6	11.5	2058	21	AAA90600	Genomic clone of 7
	28	216.6	11.5	2160	15	AAQ66160	Putative seven tra
	29	216.6	11.5	2160	19	AAV18347	Human V31 seven tr
	30	216.6	11.5	2160	21	AAA91707	Human 7TM receptor
	31	216.6	11.5	6923	22	AAK69852	Human immune/haema
	32	216	11.5	1068	24	ABK16599	DNA encoding baboo
	33	215	11.5	1137	21	AAA30729	DNA encoding human
	34	213.4	11.4	2087	22	AAK69854	Human immune/haema
	35	211.8	11.3	2154	15	AAQ64125	Epstein Barr virus
	36	211.8	11.3	2154	19	AAV22684	DNA encoding G-pro
	37	211.8	11.3	2154	19	AAV25490	cDNA for Epstein B
	38	209.8	11.2	1373	13	AAQ30013	Sequence encoding
	39	209.6	11.2	1068	24	ABK16596	DNA encoding rhesu
	40	204.8	10.9	2785	23	AAS77796	DNA encoding novel
	41	204.8	10.9	12789	24	AAS16876	Human interleukin
	42	204	10.9	6059	24	ABL32812	Human immune syste
	43	203.2	10.8	1068	17	AAA40128	Human IL-8 recepto
	44	203.2	10.8	1068	24	ABK16589	DNA encoding human
	45	203.2	10.8	1068	24	ABK16594	DNA encoding orang

ALIGNMENTS

RESULT 1
AAT72800
ID AAT72800 standard; cDNA; 1876 BP.
XX
AC AAT72800;
XX
DT 28-SEP-1997 (first entry)
XX
DE Human G-protein chemokine receptor HSATU68 cDNA.
XX
KW HSATU68; G-protein chemokine receptor; 7-transmembrane receptor;
KW signal transduction; gene therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 173..1420
FT /*tag= a
FT primer_bind complement (173..190)
FT /*tag= b
FT primer_bind 1402..1420
FT /*tag= c
XX
PN WO9725340-A1.
XX
PD 17-JUL-1997.
XX
PF 11-JAN-1996; 96WO-US00499.
XX
PR 11-JAN-1996; 96WO-US00499.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Li Y;
XX
DR WPI; 1997-372810/34.
DR P-PSDB; AAW19780.
XX
PT DNA encoding new isolated human G-protein chemokine receptor - used
PT to develop products for treating, e.g. autoimmune diseases, chronic
PT infections, allergy, malignancy, inflammation or shock
XX
PS Claim 1; Fig 1a-d; 54pp; English.
XX
CC A cDNA clone (AAT72800) codes for a newly identified human G-protein
CC chemokine receptor (AAW19780) designated HSATU68. It was identified
CC in a human genomic library derived from activated T cells. HSATU68
CC nucleic acids be used to produce HSATU68 in prokaryotic or
CC eukaryotic host cells, as probes for the detection, screening and
CC diagnosis of diseases caused by mutations in the HSATU68 gene, and
CC in the gene therapy of conditions related to underexpression of the
CC receptor its ligand.
XX
SQ Sequence 1876 BP; 343 A; 625 C; 520 G; 388 T; 0 other;

Query Match 99.9%; Score 1874.4; DB 18; Length 1876;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy       1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
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Db       1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60

Qy      61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120

Qy     121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy     181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy     241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
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Db     241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300

Qy     301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
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Db     301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy     361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
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Db     361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420

Qy     421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
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Db     421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy     481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
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Db     481 GCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy     541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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Db     541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy     601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
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Db     601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy     661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
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Db     661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720

Qy     721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy     781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy     841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy     901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy     961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy    1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
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Db    1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

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Qy    1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
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Db    1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy    1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
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Qy    1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
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Qy    1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
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Db    1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy    1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
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Qy    1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
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Db    1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy    1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
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Qy    1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
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Qy    1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
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Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
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Db   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAA 1876
          ||||||||||||||||
Db   1861 TCAGGAAAAAAAAAAA 1876
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RESULT 2
AAH35033
ID AAH35033 standard; cDNA; 1877 BP.
XX
AC AAH35033;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2115.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 8; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75628.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3596-3597; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 1877 BP; 343 A; 625 C; 518 G; 388 T; 3 other;

Query Match 99.9%; Score 1873.2; DB 22; Length 1877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1872; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
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Db      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
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Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
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Db    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
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Db    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAMTC 420

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
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Db    481 GCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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Db    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720

Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
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Db    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140

Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
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Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
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Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
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Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAA 1876
          ||||||||||||||||
Db   1861 TCAGGAAAAAAAAAAA 1876


RESULT 3
AAV26557
ID   AAV26557 standard; DNA; 1670 BP.
XX
AC   AAV26557;
XX
DT   14-AUG-1998  (first entry)
XX
DE   Human IP-10/Mig receptor CXCR3 gene.
XX
KW   ds; chemokine receptor; cellular signal; treatment; T cell;
KW   inflammatory disease; antitumour; antiviral.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             69..1175
FT                   /*tag=  a
FT                   /product= "IP-10/Mig receptor CXCR3"
FT   polyA_signal    1534..1539
FT                   /*tag=  b
FT   polyA_site      1624..1670
FT                   /*tag=  c
XX
PN   WO9811218-A1.
XX
PD   19-MAR-1998.
XX
PF   10-SEP-1997;   97WO-US15915.
XX
PR   31-MAR-1997;   97US-0829839.
PR   10-SEP-1996;   96US-0709838.
XX
PA   (KOCH-) KOCHER INST THEODOR.
PA   (LEUK-) LEUKOSITE INC.
XX
PI   Loetscher M,  Mackay CR,  Moser B,  Qin S;
XX
DR   WPI; 1998-207381/18.
DR   P-PSDB; AAW54371.
XX
PT   DNA encoding CXC chemokine receptor 3 - inhibitors and promoters of
PT   which, are useful for treatment of inflammation or in anti-tumour or
PT   anti-viral therapy
XX
PS   Claim 6; Fig 1; 137pp; English.
XX
CC   The mammalian CXC chemokine receptor 3 (CXCR3) gene encodes a protein
CC   which can selectively bind one or more chemokines and can mediate
CC   cellular signalling and/or a cellular response in response.  Inhibitors
CC   and promoters of mammalian CXCR3 can be detected and identified using
CC   host cells expressing CXCR3.  CXCR3 inhibitors can be used for treatment
CC   of inflammatory diseases which are T cell  mediated.  CXCR3 promoters are
CC   useful for antitumour or antiviral therapy.
XX
SQ   Sequence 1670 BP; 272 A; 574 C; 436 G; 388 T; 0 other;

  Query Match            82.2%;  Score 1541.6;  DB 19;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGA 1866
          ||||
Db   1618 AGGA 1621
```

RESULT 4
AAA30593
ID AAA30593 standard; cDNA; 1107 BP.
XX
AC AAA30593;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor GPR9 cDNA.
XX
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; ss.
XX
OS Homo sapiens.
XX
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
DR P-PSDB; AAY90614.
XX
PT Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
PS Example 1; Page 115; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents cDNA encoding a human wild-type
CC GPCR used in an exemplification of the invention. This was cloned and
CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC the corresponding mutant of the invention.
XX
SQ Sequence 1107 BP; 163 A; 380 C; 324 G; 240 T; 0 other;

Query Match 58.5%; Score 1097; DB 21; Length 1107;
Best Local Similarity 100.0%; Pred. No. 4.1e-234;

```
  Matches 1097;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 70

Qy     384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 130

Qy     444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 190

Qy     504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 250

Qy     564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 310

Qy     624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 370

Qy     684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     371 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 430

Qy     744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     431 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 490

Qy     804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     491 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 550

Qy     864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     551 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 610

Qy     924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     611 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 670

Qy     984 TTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 TTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 730

Qy    1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     731 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 790

Qy    1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     791 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 850

Qy    1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     851 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 910

Qy    1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     911 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 970

Qy    1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     971 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1030

Qy    1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1031 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1090

Qy    1404 CCTACTCGGGCTTGTGA 1420
           |||||||||||||||||
Db    1091 CCTACTCGGGCTTGTGA 1107


RESULT 5
AAA30714
ID   AAA30714 standard; DNA; 1107 BP.
XX
AC   AAA30714;
XX
DT   21-AUG-2000  (first entry)
XX
DE   DNA encoding human mutant G protein-coupled receptor GPR9 (M254K).
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   P-PSDB; AAY90648.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents  -
XX
PS   Example 2; Page 223; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 represent DNAs
CC   encoding the mutant human GPCRs of the invention.
XX
SQ   Sequence 1107 BP; 164 A; 380 C; 324 G; 239 T; 0 other;

  Query Match           58.4%;  Score 1095.4;  DB 21;  Length 1107;
  Best Local Similarity   99.9%;  Pred. No. 9.3e-234;
  Matches 1096;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     11 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 70

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 130

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 190

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 250

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 310

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 370

Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 430

Qy    744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 490

Qy    804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 550

Qy    864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    551 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 610

Qy    924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    611 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 670

Qy    984 TTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    671 TTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 730

Qy   1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    731 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCAAGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 790

Qy   1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    791 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 850

Qy   1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    851 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 910

Qy   1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    911 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 970

Qy   1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    971 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1030

Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1090

Qy   1404 CCTACTCGGGCTTGTGA 1420
          |||||||||||||||||
Db   1091 CCTACTCGGGCTTGTGA 1107
```

RESULT 6
AAZ32713
ID AAZ32713 standard; cDNA; 1159 BP.
XX
AC AAZ32713;
XX
DT 31-JAN-2000 (first entry)
XX
DE Human chemokine receptor CXCR3b cDNA.
XX
KW Chemokine receptor; CXCR3b; splice variant; N-terminus; CXCR3a;
KW seven transmembrane; G-protein coupled; CXC; IP10; Mig; T-lymphocyte;
KW recruitment; selective; activated; T-cell; neutrophil; inflammation;
KW tissue distribution; therapy; rheumatoid arthritis; psoriasis;
KW multiple sclerosis; transplantation; atherosclerosis; restenosis;
KW cytokine; delayed type hypersensitivity reaction; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1..52
FT /*tag= a
FT /note= "Novel exon found in CXCR3b transcripts"
FT CDS 23..1159
FT /*tag= b
FT /product= "N-terminal fragment of CXCR3b"
XX
PN WO9950299-A1.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-SE00501.
XX
PR 30-MAR-1998; 98SE-0001098.
XX
PA (ASTR) ASTRA PHARM LTD.
PA (ASTR) ASTRA AB.
XX
PI Delaney S;
XX
DR WPI; 1999-633638/54.
DR P-PSDB; AAY50129.
XX
PT New polynucleotide encoding a variant chemokine receptor -
XX
PS Claim 1; Fig 2; 18pp; English.
XX
CC This sequence represents cDNA encoding human chemokine receptor CXCR3b,
CC a splice variant of chemokine receptor CXCR3 (also referred to as
CC CXCR3a). Chemokines are a family of small cytokines which bring about the
CC recruitment of leukocytes during inflammation. The CXC chemokines
CC mostly attract neutrophils, while the CC chemokines are less selective.
CC All chemokine receptors are seven transmembrane G-protein coupled
CC receptors and most are receptors for a number of chemokines, CXCR3a
CC being a receptor for the CXC chemokines IP10 and Mig. CXCR3a is
CC expressed in activated, but not in resting T-lymphocytes, and may
CC therefore play an important role in the selective recruitment of
CC T-cells which occurs in T-cell mediated inflammatory conditions.
CC CXCR3b may have an altered pattern of tissue distribution and
CC function in the inflammatory process. Cells expressing the active
CC CXCR3b are useful for identifying ligands, especially agonists and
CC antagonists, of a chemokine receptor. In addition, the receptor
CC facilitates identification of chemokines responsible for mediating
CC inflammation reactions via interaction with CXCR3b. The modulation
CC of inflammatory responses is of therapeutic benefit in many conditions
CC such as rheumatoid arthritis, psoriasis, multiple sclerosis,
CC transplantation, delayed type hypersensitivity reactions, atherosclerosis
CC and restenosis.

```
XX
SQ   Sequence 1159 BP; 177 A; 397 C; 343 G; 242 T; 0 other;

  Query Match            58.3%;  Score 1094.6;  DB 20;  Length 1159;
  Best Local Similarity  98.3%;  Pred. No. 1.4e-233;
  Matches 1106;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy    296 GCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCC 355
          ||||    | |   ||  || |       ||||||||||||||||||||||||||||||
Db     35 GCCCACAGCCCAGGGTCACCACAGGGTTGGGTGAGTGACCACCAAGTGCTAAATGACGCC 94

Qy    356 GAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGT 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     95 GAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGT 154

Qy    416 GACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCC 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    155 GACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCC 214

Qy    476 TTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTG 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    215 TTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTG 274

Qy    536 GCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCAC 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    275 GCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCAC 334

Qy    596 CTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCC 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    335 CTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCC 394

Qy    656 GTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAAC 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    395 GTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAAC 454

Qy    716 TTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTT 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    455 TTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTT 514

Qy    776 CATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCT 835
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    515 CATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCT 574

Qy    836 GTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCAC 895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    575 GTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCAC 634

Qy    896 GACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCT 955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    635 GACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCT 694

Qy    956 CTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGC 1015
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    695 CTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTACCCCTGCTGGTCATGGCCTACTGC 754

Qy   1016 TATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATG 1075
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    755 TATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATG 814

Qy   1076 CGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTG 1135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    815 CGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTG 874

Qy   1136 GTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGC 1195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    875 GTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGC 934

Qy   1196 AGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAAC 1255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    935 AGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAAC 994

Qy   1256 CCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTG 1315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    995 CCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTG 1054

Qy   1316 CGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGAT 1375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1055 CGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGAT 1114

Qy   1376 TCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGA 1420
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1115 TCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGA 1159


RESULT 7
AAV43793
ID   AAV43793 standard; cDNA; 1620 BP.
XX
AC   AAV43793;
XX
DT   20-OCT-1998  (first entry)
XX
DE   Rodent chemokine receptor HST01.1 nucleotide sequence.
XX
KW   Chemokine; primate; human; rodent; chemokine receptor; asthma;
KW   inflammatory response; immune response; leukocyte migration; GPCR;
KW   leukocyte adhesion; chemoattractant; modulation; antiviral response;
KW   cellular morphology modification response; G-protein coupled receptor;
KW   phosphoinositide lipid turnover; abnormal proliferation; regeneration;
KW   atrophy; HST01.1; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1169
FT                   /*tag= a
FT                   /product= "chemokine receptor HST01.1"
XX
PN   WO9832858-A2.
XX
PD   30-JUL-1998.
XX
PF   22-JAN-1998;   98WO-US00902.
XX
PR   23-JAN-1997;   97US-0036715.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM,  Hedrick JA,  Mattson JD,  Soto-trejo H;
PI   Zlotnik A;
XX
DR   WPI; 1998-427954/36.
DR   P-PSDB; AAW69999.
XX
PT   Rodent and primate chemokines and chemokine receptors - useful
PT   diagnostically and therapeutically to treat conditions associated
PT   with abnormal physiology or development e.g. inflammatory conditions
XX
PS   Example 3; Pages 89-92; 105pp; English.
XX
CC   This represents a rodent chemokine receptor HST01.1 nucleotide sequence.
CC   The invention provides novel primate and rodent chemokines and chemokine
CC   receptors. The chemokines, receptors and binding compounds (optionally
CC   antibodies/fragments specifically binding the chemokines) are useful
CC   therapeutically to treat conditions associated with abnormal physiology
CC   or development e.g. inflammatory conditions such as asthma. Chemokines
CC   are important in immune and inflammatory responses in that they induce
CC   leukocyte migration and adhesion. They are also chemoattractants for
CC   several cells involved in inflammation and can induce other biological
CC   responses e.g. modulation of second messenger levels (e.g. Ca++),
CC   cellular morphology modification responses, phosphoinositide lipid
CC   turnover, possible antiviral responses etc. The chemokine receptors of
CC   the invention exhibit structural properties of G-protein coupled
CC   receptors (GPCR), although their ligands have not yet been identified.
CC   The chemokine and chemokine receptor polypeptides are useful to produce
CC   ligand:receptor complexes in vivo or in assay techniques. Assays may
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CC   also involve chemical antagonists which block complex production or
CC   utilise competitive binding.  Binding compounds identified (agonists or
CC   antagonists) can be used to modulate the physiological responses in cells
CC   (especially neurons, macrophages or lymphocytes) to treat e.g. abnormal
CC   proliferation, regeneration, generation and atrophy. The polypeptides
CC   are also used to produce antibodies useful diagnostically, for drug
CC   screening or for polypeptide purification. The polynucleotides are useful
CC   to produce probes for detecting the polypeptides, and to isolate the
CC   polypeptides or related sequences, especially from other species. They
CC   also allow transformation of cells for polypeptide production.
XX
SQ   Sequence 1620 BP; 366 A; 457 C; 405 G; 392 T; 0 other;

  Query Match             45.0%;  Score 844.4;  DB 19;  Length 1620;
  Best Local Similarity   76.6%;  Pred. No. 5.7e-178;
  Matches 1101;  Conservative    0;  Mismatches  326;  Indels   11;  Gaps    5;

Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
Db     76 AGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGCA 135

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
Db    136 CCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGCC 192

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
Db    193 CACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTCT 252

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
Db    253 TCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACTG 312

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
Db    313 CCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTGT 372

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
Db    373 TAACTCTTCCATTGTGGGCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCTGGCCTCT 432

Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
Db    433 GCAAAGTGGCAGGCGCCTTGTTCAACATCAACTTCTATGCAGGGGCCTTCCTGCTGGCTT 492

Qy    744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
Db    493 GTATAAGCTTCGACAGATATCTGAGCATAGTGCACGCCACCCAGATCTACCGCAGGGACC 552

Qy    804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
Db    553 CCCGGGTACGTGTAGCCCTCACCTGCATAGTTGTATGGGGTCTCTGTCTGCTCTTTGCCC 612

Qy    864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
Db    613 TCCCAGATTTCATCTACCTATCAGCCAACTACGATCAGCGCCTCAATGCCACCCATTGCC 672

Qy    924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
Db    673 AGTACAACTTCCCACAGGTGGGTCGCACTGCTCTGCGTGTACTGCAGCTAGTGGCTGGTT 732

Qy    984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
Db    733 TCCTGCTGCCCCTTCTGGTCATGGCCTACTGCTATGCCCATATCCTAGCTGTTCTGCTGG 792

Qy   1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
Db    793 TCTCCAGAGGCCAGAGGCGTTTTCGAGCTATGAGGCTAGTGGTAGTGGTGGTGGCAGCCT 852

Qy   1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
Db    853 TTGCTGTCTGCTGGACCCCCTATCACCTGGTGGTGCTAGTGGATATCCTCATGGATGTGG 912

Qy   1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
Db    913 GAGTTTTGGCCCGCAACTGTGGTCGAAAAAGCCACGTGGATGTGGCCAAGTCAGTCACCT 972

Qy   1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
Db    973 CGGGCATGGGGTACATGCACTGCTGCCTCAATCCGCTGCTCTATGCCTTTGTGGGAGTGA 1032

Qy   1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
Db   1033 AGTTCAGAGAGAAAATGTGGATGTTGTTCACGCGCCTGGGCCGCTCTGACCAGAGAGGGC 1092

Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
Db   1093 CCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCATCCTGGTCTGAGACAACTGAGGCCT 1152

Qy   1404 CCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTTTCGC--CCACAGTCTGACTTC 1461
Db   1153 CCTACCTGGGCTTGTAATTCTGGACTGGAACTGTAGCCTGCGCAGCCCAAGTCCTAACAC 1212

Qy   1462 CCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAATATCCTCGCTC 1521
Db   1213 ACTCCAAGTGCTTGTCCTCCTTGTAGTTGGGCTAGCTCGAACTTACCCGTAACTTTGCTG 1272

Qy   1522 CCGGGACTCACTGGCAGC-CCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCT 1580
Db   1273 CCAGGATGCACTGACAGCTCAGCATATATCCAGGTCTCCTGAGAATCAA---TTTCAGCA 1329

Qy   1581 CTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCC--GAGGT 1638
Db   1330 ACAAGGACAACACCATTACTGTGCCTTAGCTGCCATGCCCTATCTTGCTGTTTTAGAACT 1389

Qy   1639 GGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGT 1698
Db   1390 AGCTGCCTGGAGCCCCACCGCCCTACTAAATTAGCAAGTAGAACTCAGCCATCCCTGTGT 1449

Qy   1699 GCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCC 1756
Db   1450 GAGAAGAGGGAGAGGCAAATAGCACAGAGGGCCAGGCGTTGTCAGCACTGAATGTGCC 1507


RESULT 8
AAQ37107
ID   AAQ37107 standard; DNA; 1679 BP.
XX
AC   AAQ37107;
XX
DT   12-MAR-1993  (first entry)
XX
DE   New platelet factor 4 receptor superfamily member PF4ARii.
XX
KW   IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
KW   pro-inflammatory cytokine; 8rr.9; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             369..1487
FT                   /*tag= a
FT                   /product= PF4ARii
XX
PN   WO9217497-A.
XX
PD   15-OCT-1992.
XX
PF   23-MAR-1992;   92WO-US02317.
XX
PR   29-MAR-1991;   91US-0677211.
PR   19-DEC-1991;   91US-0810782.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Holmes WE,  Lee J,  Wood WI;
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XX
DR   WPI; 1992-366191/44.
DR   P-PSDB; AAR27793.
XX
PT   Isolated human platelet factor 4 super-family receptor
PT   polypeptide and corresp. antibodies and DNA - useful as
PT   diagnostic and screening agents, and for treating inflammation or
PT   PF4AR-mediated disorders
XX
PS   Claim 7; Fig 5; 78pp; English.
XX
CC   The IL-8 receptor cDNA sequence was isolated (see AAQ29505) and a
CC   874bp sub-fragment of the coding sequence was used as a probe to
CC   screen human cell line HL60 and human peripheral blood lymphocyte
CC   cDNA libraries. Two new gene sequences were found that are clearly
CC   related to the IL-8 receptor. One of these was contained in clone
CC   8rr.9 and is predicted to encode an amino acid sequence which is
CC   36% and 38% identical with the high and low affinity IL-8 receptor
CC   sequences, respectively. See also AAQ37107.
XX
SQ   Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;

  Query Match             12.8%;  Score 240;  DB 13;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 9.8e-44;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401


RESULT 9
AAQ99009
ID   AAQ99009 standard; cDNA; 1679 BP.
XX
AC   AAQ99009;
XX
DT   26-MAR-1996  (first entry)
XX
DE   Chemokine superfamily receptor coding sequence.
XX
KW   Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW   rheumatoid arthritis; inflammatory bowel disease;
KW   chronic lung inflammation; treatment; antibody;
KW   affinity purification; detection; ss.
XX
OS   Homo sapiens.
XX
PN   US5440021-A.
XX
PD   08-AUG-1995.
XX
PF   29-MAR-1991;   91US-0677211.
XX
PR   25-FEB-1994;   94US-0202056.
PR   29-MAR-1991;   91US-0677211.
XX
PA   (CHUN/) CHUNTHARAPAI A.
PA   (HEBE/) HEBERT C.
PA   (KIMK/) KIM K J.
PA   (LEEJ/) LEE J.
XX
PI   Chuntharapai A,  Hebert C,  Kim KJ,  Lee J;
XX
DR   WPI; 1995-283151/37.
DR   P-PSDB; AAR92239.
XX
PT   New antibodies against interleukin 8 type B receptor - used to treat
PT   or prevent inflammation, also for detecting receptor expression and
PT   purificn.
XX
PS   Example 2; Columns 51-54; 62pp; English.
XX
CC   Antibodies directed against the interleukin-8 receptor B can be used
CC   to treat or prevent inflammation e.g. psoriasis, dermatitis,
CC   rheumatoid arthritis and particularly inflammatory bowel disease and
CC   chronic lung inflammation.  When immobilised, these antibodies may
CC   be used to detect interleukin-8 receptor B expression in cells and
CC   tissues and for affinity purification of interleukin-8 receptor B
CC   from cells. This sequence is an additonal chemokine superfamily
CC   receptor which was identified by probing lamda libraries of genomic
CC   DNA from a human monocyte-like cell line (L-60) and human peripheral
CC   blood lymphocytes using a large fragment of the interleukin-8 type
CC   A receptor DNA (See AAQ99006).
XX
SQ   Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;

  Query Match             12.8%;  Score 240;  DB 16;  Length 1679;
  Best Local Similarity   57.0%;  Pred. No. 9.8e-44;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;
```

```
Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |   ||||||||||| |||| || |||||  || | ||
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
          |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
            |||  ||||||||||     |   ||| || ||||||||||| | | ||||||||
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || |||  |||   ||||||||  | | ||    |  | |  | |
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||  | |  ||||| | |  || | ||  | ||| | |||||  |  |||||
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
            | |  ||| | | | | |  |||| |              ||||  || |||| | ||
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |   | | |      |    ||  | ||  | |  |||||  || || ||
Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          ||||||| ||||||| |||| ||  |||| |       |  ||  |  | ||   | ||
Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
             || |||  | ||| | |  |||  |  || |||   |  ||||          |||
Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
             ||||||||||  | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
           ||  ||| |   | |||    |   |  ||    |  ||||||||   |  |
Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
            |||||||      ||||||||||||||||||  |||||||  | || |  || || ||
Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||        ||| |  ||| ||    |  ||||||||  ||  ||
Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401
```

RESULT 10
AAQ80522
ID AAQ80522 standard; cDNA; 1679 BP.
XX
AC AAQ80522;
XX
DT 18-JUL-1995 (first entry)
XX
DE Human lymphocyte PF4AR cDNA.
XX
KW Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW platelet factor superfamily receptor; lymphocyte; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 369..1487
FT /*tag= a
XX
PN WO9428931-A.
XX
PD 22-DEC-1994.
XX
PF 07-JUN-1994; 94WO-US06380.
XX
PR 11-JUN-1993; 93US-0076093.
XX
PA (GETH) GENENTECH INC.
XX
PI Chuntharapai A, Hebert C, Kim KJ, Lee J;
XX
DR WPI; 1995-036114/05.
DR P-PSDB; AAR68813.
XX
PT Treatment of inflammatory disorders - by administering an
PT antibody capable of binding a platelet factor 4 superfamily
PT receptor polypeptide
XX
PS Disclosure; Page 56-58; 83pp; English.
XX
CC 2 PF4AR members were identified by probing lambda libraries from
CC human monoclyte-like cell line HL-60 and human peripheral blood
CC lymphocytes using a large fragment of IL-8 receptor DNA (full
CC sequence given in AAQ80520). The nucleotide sequences of the 2
CC PF4ARs are given in AAQ80521 and AAQ80522, and their respective
CC amino acid sequences in AAR68812 and AAR68813.
XX
SQ Sequence 1679 BP; 327 A; 532 C; 457 G; 363 T; 0 other;

Query Match 12.8%; Score 240; DB 16; Length 1679;
Best Local Similarity 57.0%; Pred. No. 9.8e-44;
Matches 507; Conservative 0; Mismatches 365; Indels 18; Gaps 3;

```
Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |   ||||||||||| |||| || |||||  || | ||
Db    512 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 571

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db    572 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 631

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db    632 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 691

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
          |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db    692 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 751

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
            |||  ||||||||||     |   ||| || ||||||||||| | | ||||||||
Db    752 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 811

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || |||  |||   ||||||||  | | ||    |  | |  | |
Db    812 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 871

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||  | |  ||||| | |  || | ||  | ||| | |||||  |  |||||
Db    872 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 931

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
```

```
Db    932 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 991

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    992 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 1051

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db   1052 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 1111

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104

Db   1112 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 1171

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164

Db   1172 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 1231

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224

Db   1232 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1291

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db   1292 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1351

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db   1352 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1401
```

RESULT 11
AAA30626
ID AAA30626 standard; cDNA; 1119 BP.
XX
AC AAA30626;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor BLR1 cDNA.
XX
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist; ss.
XX
OS Homo sapiens.
XX
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
DR P-PSDB; AAY90627.
XX
PT Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
PS Example 1; Page 151; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents cDNA encoding a human wild-type
CC GPCR used in an exemplification of the invention. This was cloned and
CC subjected to site-directed mutagenesis (SDM) to generate DNA encoding
CC the corresponding mutant of the invention.
XX
SQ Sequence 1119 BP; 191 A; 390 C; 290 G; 248 T; 0 other;

Query Match 12.7%; Score 238.4; DB 21; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2e-43;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

```
Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    144 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 203

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    204 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 263

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642

Db    264 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 323

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    324 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 383

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    384 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 443

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    444 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 503

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    504 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 563

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930

Db    564 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 623

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    624 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 683

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db    684 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 743

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104

Db    744 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 803

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
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Db    804 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 863

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224

Db    864 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 923

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db    924 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 983

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db    984 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1033


RESULT 12
AAA30727
ID   AAA30727 standard; DNA; 1119 BP.
XX
AC   AAA30727;
XX
DT   21-AUG-2000  (first entry)
XX
DE   DNA encoding human mutant G protein-coupled receptor BLR1 (V258K).
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist; mutant; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   P-PSDB; AAY90661.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents -
XX
PS   Example 2; Page 253-254; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. Sequences AAA30709- AAA30743 and AAA30775-A30779 represent DNAs
CC   encoding the mutant human GPCRs of the invention.
XX
SQ   Sequence 1119 BP; 194 A; 389 C; 289 G; 247 T; 0 other;

 Query Match           12.7%;  Score 238.4;  DB 21;  Length 1119;
 Best Local Similarity  56.9%;  Pred. No. 2e-43;
 Matches  506;  Conservative    0;  Mismatches  366;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522

Db    144 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 203

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582

Db    204 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 263

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642

Db    264 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 323

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702

Db    324 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 383

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762

Db    384 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 443

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822

Db    444 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 503

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882

Db    504 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 563

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930

Db    564 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 623

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987

Db    624 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 683

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044

Db    684 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 743

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104

Db    744 CCAGCGGCGCCCTCAGCGGCAGAAGGCAAAAAGGGTGGCCATCCTGGTGACAAGCATCTT 803

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164

Db    804 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 863

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224

Db    864 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 923

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284

Db    924 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 983

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334

Db    984 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1033


RESULT 13
```

```
AAX87710
ID   AAX87710 standard; cDNA; 2818 BP.
XX
AC   AAX87710;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human Burkitt's lymphoma receptor 1 (BLR1) cDNA.
XX
KW   Burkitt's lymphoma receptor 1; BLR1; human;
KW   B lymphocyte chemoattractant; BLC; chemokine; ligand;
KW   drug screening; leukaemia; autoimmune disease; therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85..1203
FT                   /*tag= a
XX
PN   WO9928468-A1.
XX
PD   10-JUN-1999.
XX
PF   02-DEC-1998;   98WO-US25561.
XX
PR   02-DEC-1997;   97US-0982493.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Cyster JG,  Gunn MD,  Williams LT;
XX
DR   WPI; 1999-493764/41.
DR   P-PSDB; AAY06644.
XX
PT   Modulating interaction of a Burkitt's Lymphoma Receptor 1
PT   polypeptide and ligand, useful in drug screens
XX
PS   Example; Page 38; 42pp; English.
XX
CC   This is the nucleotide sequence of human cDNA coding for a
CC   Burkitt's lymphoma receptor 1 (BLR1, see AAY06644).  The invention
CC   relates to methods for modulating the interaction of BLR1 with
CC   its ligand, B lymphocyte chemoattractant (BLC, see AAY06642).  The
CC   methods comprise combining BLR1 and BLC polypeptides with a
CC   candidate modulator agent under conditions whereby, but for the
CC   presence of the agent, the polypeptides engage in a first
CC   interation, and determining a second interaction of the
CC   polypeptides in the presence of the agent, wherein a difference
CC   between the first and second interactions indicates that the agent
CC   modulates the interaction of the polypeptides.  The modulator is
CC   preferably an antagonist, especially dominant negative, form of
CC   BLC.  BLC and BLC agonists and antagonists may be useful for
CC   treating viral (e.g. HIV) infections, lymphoma, B lineage
CC   leukaemia, and autoimmune diseases such as rheumatoid arthritis,
CC   thyroiditis and diabetes.
XX
SQ   Sequence 2818 BP; 615 A; 874 C; 761 G; 568 T; 0 other;

  Query Match             12.7%;  Score 238.4;  DB 20;  Length 2818;
  Best Local Similarity   56.9%;  Pred. No. 2.6e-43;
  Matches  506;  Conservative    0;  Mismatches  366;  Indels   18;  Gaps    3;

Qy     463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
           |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db     228 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 287

Qy     523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
           ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db     288 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 347

Qy     583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
           ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db     348 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 407

Qy     643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
           |  || |   | ||    |||||| | ||  |   ||||||||||    |    ||||||
Db     408 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 467

Qy     703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
           |||  ||||||||||||    |   ||| || ||||||||||||  | | ||||||||
Db     468 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 527

Qy     763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
           ||||  ||| || || ||| |||   ||||||||  | | ||    |  | |   | |
Db     528 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 587

Qy     823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
           ||||||   | |  ||||| | |  || | ||  | ||| | |||||  |  ||||
Db     588 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 647

Qy     883 GTCGGCCCACCACGACGAGCGCCTCAACGC-----------CACCCACTGCCAATACAA 930
           | |  ||| | | | | |  |||| |           ||||  || |||| | ||
Db     648 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 707

Qy     931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
           |    || |   |   | | |     |    ||  | ||  | |  ||||| || || ||
Db     708 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 767

Qy     988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
           ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db     768 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 827

Qy    1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
           || |||  | ||| | |  |||  |  || |||   |  ||||       |||
Db     828 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 887

Qy    1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
           |||||||||| | ||||| ||| | ||  |  |  |||||| |||   |  |||
Db     888 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 947

Qy    1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
           ||  ||| |   | |||    |   |  ||    |  ||||||||   |  |
Db     948 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1007

Qy    1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
           |||||||      ||||||||||||||||  |||||||  | || |  || || ||
Db    1008 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067

Qy    1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
           ||||||        ||| |  ||| ||       ||||||||  ||  ||
Db    1068 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1117


RESULT 14
ABA09117/c
ID   ABA09117 standard; cDNA; 3620 BP.
XX
AC   ABA09117;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human Burkitt lymphoma receptor homologue cDNA, SEQ ID NO:893.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
```

XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11873.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
PS Claim 1; Page 779-780; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SQ Sequence 3620 BP; 708 A; 1058 C; 1076 G; 778 T; 0 other;

Query Match 12.7%; Score 238.4; DB 22; Length 3620;
Best Local Similarity 56.9%; Pred. No. 2.8e-43;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

```
Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db   3393 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 3334

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | ||| | | |  |||    | |  ||   ||| || ||
Db.  3333 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 3274

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   |||||||  | |   |||| |   |
Db   3273 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 3214

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
          |  || |   | ||    |||||| | ||  |  ||||||||||   |    ||||||
Db   3213 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 3154

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
          |||  ||||||||||    |   ||| || ||||||||||||  | | ||||||||
Db   3153 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 3094

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || ||| |||  ||||||||  | | ||   |  | |   | |
Db   3093 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 3034

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||   | |  ||||| | |  || | ||  | ||| | |||||  |  |||||
Db   3033 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 2974

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
            | |  ||| | | | |  |||| |            ||||  || |||| | ||
Db   2973 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 2914

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |   | | |     |    ||  | ||  | |  ||||| || || ||
Db   2913 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 2854

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db   2853 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 2794

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
            || |||  | ||| | |  |||  |  || |||   |  ||||          |||
Db   2793 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 2734

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
          ||||||||||  | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db   2733 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 2674

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
            || ||| |   | |||    |   |  ||    |   ||||||||   |  |
Db   2673 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 2614

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
          |||||||      |||||||||||||||||  |||||||  | || |  || || ||
Db   2613 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 2554

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||       ||| |  ||| ||       ||||||||  ||  ||
Db   2553 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 2504
```

RESULT 15
AAQ30011
ID AAQ30011 standard; cDNA; 1200 BP.
XX
AC AAQ30011;
XX
DT 04-APR-1993 (first entry)
XX
DE Sequence encoding a high affinity recombinant rabbit interleukin-8
DE (IL-8) receptor polypeptide in F3R.
XX
KW IL-8 receptor polypeptide; G-protein-coupled receptor; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers

```
FT   CDS             108..1172
FT                   /*tag=  a
XX
PN   WO9218641-A.
XX
PD   29-OCT-1992.
XX
PF   10-APR-1992;   92WO-US02977.
XX
PR   10-APR-1991;   91US-0685101.
PR   09-JUL-1991;   91US-0726606.
PR   09-DEC-1991;   91US-0803842.
XX
PA   (REPK ) REPLIGEN CORP.
PA   (UYBO-) UNIV BOSTON.
XX
PI   Navarro J,  Thomas KM,  Witt DP;
XX
DR   WPI; 1992-382123/46.
DR   P-PSDB; AAR28272.
XX
PT   Recombinant mammalian interleukin-8 receptor - used for screening
PT   interleukin-8 binding antagonists, used to treat inflammation
XX
PS   Disclosure; Fig 1; 71pp; English.
XX
CC   Rabbit high affinity IL-8 receptor gene was isolated from rabbit
CC   peritoneal neutrophils and used as a source of poly(A)+ RNA, to
CC   produce a rabbit neutrophil cDNA library.  250,000 recombinant
CC   plaques were screened for those which hybridized to an antisense
CC   oligonucleotide (AAQ30015).  This probe was designed based on the
CC   sequence derived from the second transmembrane domain of G-protein-
CC   coupled receptors.  After tertiary screening, six plaques were
CC   isolated.  The insert of one of these plaques, termed F3R was of 2.5
CC   kb in size.  This insert was sequenced.  The protein deduced from
CC   the F3R clone demonstrates that it belongs to the family of
CC   G-protein-coupled receptors.  The deduced protein sequence
CC   indicates seven putatuve transmembrane segments.
XX
SQ   Sequence 1200 BP; 234 A; 366 C; 294 G; 304 T; 2 other;

  Query Match             12.3%;  Score 231;  DB 13;  Length 1200;
  Best Local Similarity   55.5%;  Pred. No. 8.9e-42;
  Matches  491;  Conservative    0;  Mismatches  385;  Indels    9;  Gaps    2;

Qy    446 CAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTT 505
Db    213 CTGGTAGTCACCCAGACACTTAACAAATATGTTGTGGTCGTCATCTATGCCCTGGTCTTC 272

Qy    506 CTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCC 565
Db    273 CTGCTGAGCCTGCTGGGCAACTCCCTGGTGATGCTGGTCATACTGTACAGCCGGAGCAAC 332

Qy    566 CTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTG 625
Db    333 CGTTCGGTCACCGACGTCTACCTGCTGAACCTGGCCATGGCCGACCTGCTTTTTGCCCTG 392

Qy    626 ACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGC 685
Db    393 ACCATGCCTATCTGGGCCGTCTCCAAGGAAAAAGGCTGGATTTTCGGCACGCCCCTGTGC 452

Qy    686 AAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGC 745
Db    453 AAGGTGGTCTCGCTTGTGAAGGAAGTCAACTTCTACAGTGGAATCCTGCTCCTGGCCTGC 512

Qy    746 ATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCC 805
Db    513 ATCAGTGTGGACCGCTACCTGGCCATTGTCCATGCTACTCGCACACTGACCCAGAAGCGC 572

Qy    806 CCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTC 865
Db    573 C---ACTTGGTCAAGTTCATATGTCTGGGCATCTGGGCGCTGTCTCTGATTTTGTCCCTG 629

Qy    866 CCAGACTTCATCTTCC------TGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCAC 919
Db    630 CCCTTCTTCCTCTTCCGCCAAGTCTTTTCTCCAAACAATTCCAGCCCGGTCTGCTATGAG 689

Qy    920 TGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCT 979
Db    690 GACCTGGGTCACAACACAGCGAAATGGCGCATGGTGCTGCGGATCCTGCCACACACTTTC 749

Qy    980 GGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG 1039
Db    750 GGCTTCATCCTGCCGCTGCTGGTCATGCTGTTTTGCTATGGGTTCACCCTGCGCACGCTG 809

Qy   1040 CTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTG 1099
Db    810 TTCCAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGGTCATCTTCGCCGTCGTGCTC 869

Qy   1100 GCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGAC 1159
Db    870 ATCTTCCTTCTCTGCTGGCTGCCCTACAACCTGGTCCTGCTCGCAGACACCCTCATGAGG 929

Qy   1160 CTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTC 1219
Db    930 ACCCACGTGATCCAGGAGACGTGTCAGCGTCGCAATGACATTGACCGGGCCCTGGACGCC 989

Qy   1220 ACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGG 1279
Db    990 ACCGAGATTCTGGGCTTCCTGCACAGCTGCCTCAACCCCATCATCTACGCCTTCATTGGC 1049

Qy   1280 GTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGC 1324
Db   1050 CAAAACTTTCGCAATGGATTCCTCAAGATGCTTGCGGCCCGCGGC 1094


Search completed: November  2, 2002, 04:24:01
Job time : 250 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 04:19:52 ; Search time 1671 Seconds
(without alignments)
15152.775 Million cell updates/sec

Title: US-09-101-518A-1
Perfect score: 1876
Sequence: 1 cctgaagggagagcagggag.....atcgtcaggaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	729.6	38.9	864	10	BI911171	BI911171 603062744
2	726.6	38.7	851	10	BI768435	BI768435 603053902
3	655	34.9	749	10	BI821147	BI821147 603035039
c 4	493.6	26.3	617	9	AI587350	AI587350 tr81c12.x
5	398.8	21.3	578	10	BI975807	BI975807 484335 MA
6	385.8	20.6	471	9	AW655246	AW655246 106015 MA
7	339.4	18.1	348	9	AJ346279	AJ346279 sHr-00001
8	273	14.6	468	10	BF452722	BF452722 maa56a05.
9	269.8	14.4	511	10	BE589641	BE589641 195994 BA
c 10	263	14.0	708	10	BF453946	BF453946 maa56a05.
11	239	12.7	392	9	AW354767	AW354767 36085 MAR
12	162.8	8.7	871	10	BI653693	BI653693 603300354
13	161.2	8.6	944	9	AL523112	AL523112 AL523112
c 14	158.4	8.4	573	10	BI395190	BI395190 TUDPEc185
15	155	8.3	935	9	AL531903	AL531903 AL531903
16	152.2	8.1	765	10	BM387369	BM387369 UI-R-CN1-
17	151.4	8.1	910	10	BI762229	BI762229 603049139
18	147.6	7.9	604	9	BB637479	BB637479 BB637479
19	147.4	7.9	543	10	BI540027	BI540027 452946 MA
c 20	144	7.7	674	10	BM251350	BM251350 BOTL01000
21	143.4	7.6	827	10	BI761664	BI761664 603046395
22	142.8	7.6	891	10	BI824663	BI824663 603033815
23	142.6	7.6	841	9	AL558854	AL558854 AL558854
24	141.6	7.5	971	9	AU091121	AU091121 AU091121
25	140.6	7.5	672	9	AL631373	AL631373 AL631373
26	140.4	7.5	529	9	AW653917	AW653917 102840 MA
27	139.4	7.4	668	9	AL660726	AL660726 AL660726
28	137	7.3	857	10	BG682791	BG682791 602651283
29	136	7.2	750	10	BG613352	BG613352 602641234
30	135.4	7.2	575	10	BM035806	BM035806 fu20e08.y
c 31	134.2	7.2	555	9	AI234161	AI234161 EST230849
32	134	7.1	549	10	BE751067	BE751067 202785 MA
33	133.4	7.1	746	10	BI917014	BI917014 603177688
34	133.2	7.1	875	10	BI756157	BI756157 603030061
35	132.2	7.0	905	10	BI754094	BI754094 603027651
36	132	7.0	914	10	BI822179	BI822179 603039895
37	131.4	7.0	549	10	BF045645	BF045645 BP250005A
c 38	131.4	7.0	556	12	AZ340465	AZ340465 1M0072B02
39	131.4	7.0	742	10	BI597875	BI597875 603245357
40	130	6.9	702	10	BI761118	BI761118 603043593
41	129.4	6.9	658	10	BI835125	BI835125 603087792
42	129.4	6.9	671	10	BG025793	BG025793 602274794
43	129.4	6.9	703	10	BI765768	BI765768 603046522
44	129.4	6.9	728	9	AU117058	AU117058 AU117058
45	129.4	6.9	782	10	BG685901	BG685901 602638730

ALIGNMENTS

RESULT 1
BI911171
LOCUS BI911171 864 bp mRNA linear EST 16-OCT-2001
DEFINITION 603062744F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212066 5', mRNA sequence.
ACCESSION BI911171
VERSION BI911171.1 GI:16174778
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 864)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11532 row: g column: 11
High quality sequence start: 3
High quality sequence stop: 788.
FEATURES Location/Qualifiers
source 1. .864
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/db_xref="taxon:9606"
/clone="IMAGE:5212066"
/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
BASE COUNT 133 a 306 c 246 g 179 t
ORIGIN

Query Match 38.9%; Score 729.6; DB 10; Length 864;
Best Local Similarity 95.5%; Pred. No. 4.7e-142;
Matches 783; Conservative 0; Mismatches 34; Indels 3; Gaps 3;

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Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     39 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 98

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     99 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 158

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    159 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 218

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    219 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 278

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    279 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 338

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
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Db    339 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 398

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db    399 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 458

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    459 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 518

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
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Db    519 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 578

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
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Db    579 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 638

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    639 GCCTCAACGCCA-CCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 697

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    698 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATG-CC 756

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGC-GGCGCCTGCGGGCCATGCGGCTG 1081
          |||||||||||||||||||||||||||||||||| ||||||||| |||||||| |||
Db    757 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGGCGCCTGCAGGCCATGCTGCTT 816

Qy   1082 GTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCC 1121
          |  |    ||    ||  | |||||| ||||  |  |||
Db    817 GGTGGTAGGGAGCCGGGTGGCTTTGCCGTCTGTGGACCCC 856
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RESULT 2
BI768435
LOCUS BI768435 851 bp mRNA linear EST 25-SEP-2001
DEFINITION 603053902F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203512 5', mRNA sequence.
ACCESSION BI768435
VERSION BI768435.1 GI:15760013
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11510 row: c column: 01
High quality sequence stop: 801.
FEATURES Location/Qualifiers
source 1. .851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5203512"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."
BASE COUNT 128 a 305 c 240 g 178 t
ORIGIN

Query Match 38.7%; Score 726.6; DB 10; Length 851;
Best Local Similarity 96.5%; Pred. No. 2e-141;
Matches 796; Conservative 0; Mismatches 24; Indels 5; Gaps 5;

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Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     29 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 88

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Db     89 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 148

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 208

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    209 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 268

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    269 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 328

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    329 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 388

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db    389 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 448

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
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Db    449 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 508

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    509 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 568

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCA-CGACGAG 901
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    569 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCAGCGACGAG 628

Qy    902 CGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGG 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    629 CGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGG 688

Qy    962 GTGCTGCAGCTGGTGGCTGGCTTTC-TGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          |||||||||||||||||||||||| |||||||||||||||||||||||  |||||
Db    689 GTGCTGCAGCTGGTGGCTGGCTTTCTTGCTGCCCCTGCTGGTCATGGCCTACTTGTATGC 748

Qy   1021 CCACATCCTGGCC-GTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGC 1079
          |||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Db    749 CCACATCCTGGCCTGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGG-CATGCGGC 807

Qy   1080 TGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCT 1124
          | |||||||| | |   |  | ||||||||||| ||||||||||
Db    808 T-GTGGTGGTAGGCAGTGGTGGCTTTGCCCTCTGGTGGACCCCCT 851


RESULT 3
BI821147
LOCUS       BI821147                749 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603035039F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176136 5',
            mRNA sequence.
ACCESSION   BI821147
VERSION     BI821147.1  GI:15932697
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 749)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11438  row: n  column: 09
            High quality sequence stop: 747.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      121 a    274 c    201 g    153 t
ORIGIN

  Query Match             34.9%;  Score 655;  DB 10;  Length 749;
  Best Local Similarity   97.5%;  Pred. No. 1.7e-126;
  Matches  697;  Conservative    0;  Mismatches   15;  Indels    3;  Gaps    3;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     28 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 87

Qy    363 CCGCCCTCCTGGAGAACTTCA-GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCG 421
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db     88 CCGCCCTCCTGGAGAACTTCAGGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCG 147

Qy    422 TGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTG 481
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 TGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTG 207

Qy    482 CCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCC 541
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Db    208 CCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCC 267

Qy    542 GTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCT 601
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Db    268 GTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCT 327

Qy    602 GTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAG 661
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Db    328 GTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAG 387

Qy    662 TGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTAC 721
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Db    388 TGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTAC 447

Qy    722 GCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCC 781
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Db    448 GCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCC 507

Qy    782 ACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGG 841
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 ACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGG 567

Qy    842 GGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAG 901
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Db    568 GGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAG 627

Qy    902 CGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGC-G 960
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Db    628 CGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGG 687

Qy    961 GGTGCTGCAGCTGGTGGC-TGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTG 1014
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Db    688 GGTGCTGCAGCTGGTGGCTTGGCTTTCTGCTGCCCCTGCTGGTCATGGCTAACTG 742


RESULT 4
AI587350/c
LOCUS       AI587350                617 bp    mRNA    linear   EST 14-MAY-1999
DEFINITION  tr81c12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224726 3'
            similar to SW:CCR3_HUMAN P49682 C-X-C CHEMOKINE RECEPTOR TYPE 3 ;,
            mRNA sequence.
ACCESSION   AI587350
VERSION     AI587350.1  GI:4573791
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1908   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 180
            POLYA=No.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2224726"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT      141 a    145 c    200 g    124 t      7 others
ORIGIN

  Query Match             26.3%;  Score 493.6;  DB 9;  Length 617;
  Best Local Similarity   92.4%;  Pred. No. 8.2e-93;
  Matches  570;  Conservative    0;  Mismatches   41;  Indels    6;  Gaps    5;

Qy   1265 TATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG-ATGTGGATGCTGCTC-TTGCGCCTGG 1322
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Db    617 TATGCCTTTGTAGGGGCAAGTTTCCGGGAACGGAATGTGGATGCTGCTCTTTGCGCCTGG 558

Qy   1323 GCTGCCCCAACCAGAGA--GGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
           |    ||| |||||| |  |||||||||||||||||||||   ||||  ||||||||||||
Db    557 GGCTGCCCCACCAGAAAAGGGGCTCCAGAGGCAGCCATCTCTTTCCGCCCGGGATTCATC 498

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
             ||| |||  |     ||||||||||||||||||||||||||||||||||||||||||
Db    497 TGGGTTTGAACCTCAGAAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 438

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
           |||||||||||| | || |||| ||||| ||||||||||  |||| |||||| | |||
Db    437 TTTCGCCCACAGTTTNACCTCCCGGCATTNCAGGCTCCTCCTCCCCTTTGCCGGNTNTGG 378

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    377 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACC-CCAGGTCTCCC 319

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
           |||||||||||||||||| |||||| |||||||||| ||||||||||||||||||||||
Db    318 GGGAAGCCACCCTCCCAGCTTTGAGGANTGCACCATTGNTGCTCCTTAGCTGCCAAGCCC 259

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAG-CCCCACTGCCCTTCTCATTTGGAAACTAA 1679
           |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db    258 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCCACNGCCCTTCTCATTTGGAAACTAA 199

Qy   1680 AACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 AACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATG 139

Qy   1740 AAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTA 1799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 AAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTA 79

Qy   1800 TATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATC 1859
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 TATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATC 19

Qy   1860 GTCAGGAAAAAAAAAAAA 1876
           ||||||||||||||||||
Db     18 GTCAGGAAAAAAAAAAAA 2


RESULT 5
BI975807
LOCUS       BI975807                 578 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  484335 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI975807
VERSION     BI975807.1  GI:16350212
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 110  row: A  column: 16
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .578
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 2BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, thymus,
                     semitendonosus muscle, longissimus muscle, pancreas,
                     adrenal, and endometrium."
BASE COUNT       92 a    199 c    152 g    135 t
ORIGIN

  Query Match             21.3%;  Score 398.8;  DB 10;  Length 578;
  Best Local Similarity   82.7%;  Pred. No. 5e-73;
  Matches  470;  Conservative    0;  Mismatches   92;  Indels    6;  Gaps    1;

Qy    299 CCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAG 358
          | | ||  |||       |  | |  || ||||||| | ||||| | |  | | | ||||
Db     17 CGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGAT 76

Qy    359 GTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAC 418
           |||||  |||||||||| ||      |||||||||||||| |||||||| ||||   ||
Db     77 TTTGCCTACCTCCTGGAAAA------CTCTTCCTATGACTACGGAGAAAATGAGACCTAC 130

Qy    419 TCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTC 478
          |  |||||||| ||||| |||||||||||||||||||||| ||||||||||  |||||
Db    131 TTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTC 190

Qy    479 CTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCA 538
          ||||| | |||||||||||||||||| |||||||||| ||||| || |||   ||||||
```

```
Db    191 CTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTGGGTAATGGCATCGTGGCA 250

Qy    539 GCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTA 598
          | |||||||||||||| | || | ||||||||||||||||||||||| ||||| ||| |
Db    251 GTCGTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGACACCTTTCTGCTGCACTTG 310

Qy    599 GCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTC 658
          ||||| || ||  | |||||||||||||||| || ||||||||||||| || ||| ||
Db    311 GCTGTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGGGCAGTGGATGCAGCCATC 370

Qy    659 CAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTC 718
          |||||||||||||||||||||||||||||||||| |||| ||||||||||||||||||
Db    371 CAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCGGGTGCACTCTTCAACATCAACTTC 430

Qy    719 TACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCAT 778
          |||||||| |||||||||||||||| |||||||| || || ||||||| ||| || ||
Db    431 TACGCAGGGGCCCTCCTGCTGGCCTGTATCAGCTTCGATCGGTACCTGAGCATTGTGCAC 490

Qy    779 GCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTC 838
          |||||||||||||||||||||||| |||||| | |||||| |||||||||  |||| |||
Db    491 GCCACCCAGCTCTACCGCCGGGGCCCCCCGACTCGCGTGGCCCTCACCTGTGTGGCAGTC 550

Qy    839 TGGGGGCTCTGCCTGCTTTTCGCCCTCC 866
          |||||||||| ||||| || || ||||
Db    551 TGGGGGCTCTGTCTGCTCTTTGCGCTCC 578


RESULT 6
AW655246
LOCUS       AW655246                471 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  106015 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW655246
VERSION     AW655246.1  GI:7421144
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 86  row: D  column: 24
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."

BASE COUNT       72 a    152 c    148 g     99 t
ORIGIN

  Query Match            20.6%;  Score 385.8;  DB 9;  Length 471;
  Best Local Similarity  88.9%;  Pred. No. 2.5e-70;
  Matches  417;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy    900 AGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGC 959
          | |||||||| |||||||||||||| |||||||||||||||| ||||| ||| |||||||
Db      3 ACCGCCTCAATGCCACCCACTGCCAGTACAACTTCCCACAGGAGGGCCACACAGCTCTGC 62

Qy    960 GGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATG 1019
          |  | |||||||||||||| ||||| |||||||||||||||||||||||||| |||||||
Db     63 GCATCCTGCAGCTGGTGGCAGGCTTCCTGCTGCCCCTGCTGGTCATGGCCTATTGCTATG 122

Qy   1020 CCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGC 1079
          ||| ||||||||| |||||||||| |||||||||||||||||  |  | ||||||||||
Db    123 CCCGCATCCTGGCTGTGCTGCTGGTCTCCAGGGGCCAGCGGCGGCTCAGAGCCATGCGGC 182

Qy   1080 TGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGC 1139
          |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db    183 TGGTGGTGGTGGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTACCACCTGGTGGTGC 242

Qy   1140 TGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGG 1199
          ||||||||| |||||||||||||| || || ||||| ||||| ||| |||||||||| |
Db    243 TGGTGGACACCCTCATGGACCTGGGGGCCTTAGCCCGTAACTGCGGCAGAGAAAGCAGTG 302

Qy   1200 TAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGC 1259
          | ||| | |||||||||||||| || ||| ||||||||||||||||||||||||||||| |
Db    303 TGGACATAGCCAAGTCGGTCACGTCGGGCATGGGCTACATGCACTGCTGCCTCAACCCAC 362

Qy   1260 TGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCC 1319
          |||||||||||||||| || |||||||||| |||||||||| |||| ||| |||| |
Db    363 TGCTCTATGCCTTTGTGGGTGTCAAGTTCCGAGAGCGGATGTGGGTGCTACTCGTGCGTC 422

Qy   1320 TGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCG 1368
          ||||||||||  |||||||  | | |||| |||||||||  |||||||
Db    423 TGGGCTGCCCTGACCAGAGGTGCCACCAGCGGCAGCCATCAGCTTCCCG 471


RESULT 7
AJ346279
LOCUS       AJ346279                348 bp    mRNA    linear   EST 14-AUG-2001
DEFINITION  sHr-000016-0-E11 HM3/S3 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AJ346279
VERSION     AJ346279.1  GI:15167462
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Laveder,P., De Pitta,C., Toppo,S., Valle,G. and Lanfranchi,G.
  TITLE     Specific subtraction of abundant mRNAs in skeletal muscle
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Laveder P
            CRIBI Biotechnology Centre
            University of Padua
            Via U. Bassi 58/B, 35121 Padua, Italy
            sequencing centre identifier: HSPD50322
             ABI Chromatograms and other information are available on WWW at
            http://muscle.cribi.unipd.it
            Seq primer: PC2R.
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="HM3/S3"
                     /sex="female"
                     /tissue_type="pectoral muscle (after mastectomy)"
                     /note="Vector: p0PD (Custom); Site_1: EcoRI; Site_2: NotI;
                     caucasian; Skeletal muscle cDNA was depleted of hundred
                     most expressed mRNAs through an original two steps
```

subtractive procedure"
BASE COUNT 87 a 110 c 74 g 77 t
ORIGIN

Query Match 18.1%; Score 339.4; DB 9; Length 348;
Best Local Similarity 99.7%; Pred. No. 1.2e-60;
Matches 340; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   1536 CAGCCCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCA 1595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7 CAGCCCCAGCACCACCAGGTCTCCCGGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCA 66

Qy   1596 TTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCA 1655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 TTGCTGCTCCTTAGCTGCCAAGCCCCATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCA 126

Qy   1656 CTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCA 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 CTGCCCTTCTCATTTGGAAACTAAAACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCA 186

Qy   1716 TGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTG 1775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 TGGCGTAGAGGGTGCTGCCCCATGAAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTG 246

Qy   1776 TGGCCATGGTCCCCAAGACCTCTATATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCT 1835
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    247 TGGCCATGGTCCCCAAGACCTCTATATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCT 306

Qy   1836 TAAAACTTTTCAATAAACAAGATCGTCAGGAAAAAAAAAAA 1876
          |||||||||||||||||||||||||||||||||||||||||
Db    307 TAAAACTTTTCAATAAACAAGATCGTCAGGAAAAAAAAAAA 347
```

RESULT 8
BF452722
LOCUS BF452722 468 bp mRNA linear EST 01-DEC-2000
DEFINITION maa56a05.y1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3820689 5' similar to TR:O88410 O88410 CHEMOKINE RECEPTOR CXCR3. [1] ;, mRNA sequence.
ACCESSION BF452722
VERSION BF452722.1 GI:11518891
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 468)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1457041
Seq primer: -40RP from Gibco
High quality sequence stop: 382.
FEATURES Location/Qualifiers
source 1. .468
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3820689"
/clone_lib="Soares mouse 3NbMS"
/sex="male"
/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through three rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 90 a 143 c 119 g 116 t
ORIGIN

Query Match 14.6%; Score 273; DB 10; Length 468;
Best Local Similarity 80.9%; Pred. No. 8.8e-47;
Matches 331; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

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Qy    324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
          |||| ||||| |  |||||||||| ||| | | ||  |||||   || ||||| |||  ||
Db     62 AGGTTAGTGAACGTCAAGTGCTAGATGCCTCGGACTTTGCCTTTCTTCTGGAAAACAGCA 121

Qy    384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
          |||| |||| || ||||| |||||||||| |||   | || |  ||||||||||||||
Db    122 CCTCTCCCTACGATTATGGGGAAAACGAGAGCGAC---TTCTCTGACTCCCCGCCCTGCC 178

Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
          ||||||| |||||||||||||| ||| |  ||||||||||||||||||||||||||||||
Db    179 CACAGGATTTCAGCCTGAACTTTGACAGAACCTTCCTGCCAGCCCTCTACAGCCTCCTCT 238

Qy    504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
          |  |||||||||||| ||||| || |||||||| || ||||| ||||| | ||| || |
Db    239 TCTTGCTGGGGCTGCTAGGCAATGGGGCGGTGGCTGCTGTGCTACTGAGTCAGCGCACTG 298

Qy    564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
          |||||||||||| |||||||||||||||||||| |||||||| ||    |||||||||
Db    299 CCCTGAGCAGCACGGACACCTTCCTGCTCCACCTGGCTGTAGCCGATGTTCTGCTGGTGT 358

Qy    624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
          | || || ||  | |||||||||| ||||| |||||||||| || ||| || ||||||
Db    359 TAACTCTTCCATTGTGGGCAGTGGATGCTGCTGTCCAGTGGGTTTTCGGCCCTTGCCTCT 418

Qy    684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCT 732
          |||||||||| | ||| | |||||||| ||||| || | | | ||| |
Db    419 GCAAAGTGGCAAGCGCCTTGTTCAACATTAACTTTTATGTAAGGGCCTT 467
```

RESULT 9
BE589641
LOCUS BE589641 511 bp mRNA linear EST 28-AUG-2000
DEFINITION 195994 BARC 5BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE589641
VERSION BE589641.1 GI:9842680
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 511)
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassell,C.P., Ashwell,M.S. and Wells,K.D.
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 122 row: N column: 12

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          Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .511
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="BARC 5BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled mRNA isolated from mammary
                     tissues at eight physiological, developmental, and disease
                     states."
BASE COUNT       97 a    167 c    135 g    112 t
ORIGIN

  Query Match             14.4%;  Score 269.8;  DB 10;  Length 511;
  Best Local Similarity   80.8%;  Pred. No. 4.1e-46;
  Matches  329;  Conservative    0;  Mismatches   72;  Indels    6;  Gaps    1;

Qy     299 CCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAG 358
           | | ||  |||      |  | |  || ||||||| | ||||| | |  | | | ||||
Db     111 CGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGAT 170

Qy     359 GTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAC 418
           |||||  |||||||||  ||      ||||||||||||||| |||||||| ||||   ||
Db     171 TTTGCCTACCTCCTGGAAAA------CTCTTCCTATGACTACGGAGAAAATGAGACCTAC 224

Qy     419 TCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTC 478
           |  ||||||| ||||| |||||||||||||||||||||| ||||||||||  |||||
Db     225 TTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTC 284

Qy     479 CTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCA 538
           ||||| | |||||||||||||||||| |||||||||| ||||| || |||   ||||||
Db     285 CTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTGGGTAATGGCATCGTGGCA 344

Qy     539 GCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTA 598
           | |||||||||||||| | || | |||||||||||||||||||||||| ||||| ||| |
Db     345 GTCGTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGACACCTTTCTGCTGCACTTG 404

Qy     599 GCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTC 658
           ||||| || ||  | |||||||||||||||| || |||||||||||||| || ||| ||
Db     405 GCTGTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGGGCAGTGGATGCAGCCATC 464

Qy     659 CAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTT 705
           |||||||||||||||||||||||||||||||| ||||| |||||
Db     465 CAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCGGGTGCACTCTT 511


RESULT 10
BF453946/c
LOCUS       BF453946                 708 bp    mRNA    linear   EST 01-DEC-2000
DEFINITION  maa56a05.x1 Soares mouse 3NbMS Mus musculus cDNA clone
            IMAGE:3820689 3' similar to TR:O88410 O88410 CHEMOKINE RECEPTOR
            CXCR3. [1] ;, mRNA sequence.
ACCESSION   BF453946
VERSION     BF453946.1  GI:11520115
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Other_ESTs: maa56a05.y1
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1457041
            High quality sequence stop: 444.
```

```
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3820689"
                     /clone_lib="Soares mouse 3NbMS"
                     /sex="male"
                     /tissue_type="Spleen"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTGTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through
                     three rounds of normalization, and was constructed by
                     Bento Soares and M.Fatima Bonaldo."
BASE COUNT      172 a    173 c    185 g    178 t
ORIGIN

  Query Match             14.0%;  Score 263;  DB 10;  Length 708;
  Best Local Similarity   68.6%;  Pred. No. 1.1e-44;
  Matches  422;  Conservative    0;  Mismatches  185;  Indels    8;  Gaps    4;

Qy    1139 CTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGG 1198
           || ||||| ||| ||||||| |||| | ||||||||||||||||| |||||||||
Db     708 CTAGTGGATATCTTCATGGATGTGGGAGTTTTGGCCCGCAACTGTGGTCGAGAAAGCCAC 649

Qy    1199 GTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCG 1258
           || || |||||||||| |||||||| ||| |||| |||||||||| |||||||| |||
Db     648 GTGGATGTGGCCAAGTCAGTCACCTCGGGCATGGGGTACATGCACTGTTGCCTCAATCCG 589

Qy    1259 CTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGC 1318
           |||||||||||||||| || || |||||| | ||||  |||||||| || ||  ||||
Db     588 CTGCTCTATGCCTTTGTGGGAGTGAAGTTCAGAGAGCAAATGTGGATGTTGTTCACGCGC 529

Qy    1319 CTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCA 1378
           |||||| || |  |||||||||||| |||| ||||||| || ||||| ||  | || |||
Db     528 CTGGGCCGCTCTGACCAGAGAGGGCCCCAGCGGCAGCCGTCATCTTCACGGAGAGAATCA 469

Qy    1379 TCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCC 1438
           |||||||||||||  | ||||||||||||  ||||||||  |  | |||  |
Db     468 TCCTGGTCTGAGACAACTGAGGCCTCCTACCTGGGCTTGTAATTCTGGACTGGAACTGTA 409

Qy    1439 CCTTTCGC--CCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCT 1496
           | | |||  ||  ||||  |   | |  ||         ||||||  |     ||
Db     408 GCCTGCGCAGCCCAAGTCCTAACACACTCCAAGTGCTTGTCCTCCTTGTAGTTGGGCTAG 349

Qy    1497 CTGGCTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGC-CCCAGCACCACCAGGT 1555
           || |  ||  ||  || | | ||| || |||  ||||| |||| |     |   ||||||
Db     348 CTCGAACTTACCCGTAACTTTGCTGCCAGGATGCACTGACAGCTCAGCATATATCCAGGT 289

Qy    1556 CTCCCGGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCA 1615
           |||| | ||| | |   || ||||    |||||  ||||||| |||  ||||||||||||
Db     288 CTCCTGAGAATCAA---TCTCAGCAACAAGGACAACACCATTACTGTGCCTTAGCTGCCA 232

Qy    1616 AGCCCCATCCTGCCGCCCGAGG--TGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGA 1673
           |||| ||| ||| |     ||   | |||||||||||||| | ||||| || | || |
Db     231 TGCCCTATCTTGCTGTTTTAGAACTAGCTGCCTGGAGCCCCCCCGCCCTACTAAATTAGC 172

Qy    1674 AACTAAAACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGC 1733
           || || ||||    | ||||   ||| |  |||    |||||     | | || | ||
Db     171 AAGTAGAACTCAGCCATCCCTGTGTGAGAAGAGGGAGAGGCAAATAGCACAGAGGGCCAG 112

Qy    1734 CCCATGAAGCCACAG 1748
           |  ||    ||| |
Db     111 GCGTTGTCAGCACTG 97
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RESULT 11
AW354767
LOCUS       AW354767               392 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  36085 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW354767
VERSION     AW354767.1  GI:6853757
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 23  row: J  column: 5
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT       70 a    131 c    102 g     89 t
ORIGIN

  Query Match             12.7%;  Score 239;  DB 9;  Length 392;
  Best Local Similarity   79.6%;  Pred. No. 1.1e-39;
  Matches  297;  Conservative    0;  Mismatches   70;  Indels    6;  Gaps    1;

Qy    299 CCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAG 358
          | | ||  |||      |  | |  || ||||||| | ||||| | |  | | | ||||
Db     26 CGTACCAGCCCAGCTATGGTCCCTGAGATGAGTGAACGCCAAGAGTTCCAAGCCTCCGAT 85

Qy    359 GTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAC 418
           |||||  ||||||||| ||      |||||||||||||| |||||||| ||||   ||
Db     86 TTTGCCTACCTCCTGGAAAA------CTCTTCCTATGACTACGGAGAAAATGAGACCTAC 139

Qy    419 TCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTC 478
          |  |||||||| ||||| ||||||||||||||||||||| |||||||||||  |||||
Db    140 TTCTGCTGTACTTCCCCACCCTGCCCACAGGACTTCAGCCTCAACTTCGACCGCACCTTC 199

Qy    479 CTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCA 538
          ||||| | ||||||||||||||||||| |||||||||| ||||| || |||   ||||||
Db    200 CTGCCCGTCCTCTACAGCCTCCTCTTTGTGCTGGGGCTTCTGGGTAATGGCATCGTGGCA 259

Qy    539 GCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTA 598
          | |||||||||||||| | || | |||||||||||||||||||||| ||||| ||| |
Db    260 GTCGTGCTGCTGAGCCAGAGGGCGGCCCTGAGCAGCACCGACACCTTTCTGCTGCACTTG 319

Qy    599 GCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTC 658
          ||||| || ||  | |||||||||||||||| || |||||||||||||| || ||| ||
Db    320 GCTGTGGCCGATGCACTGCTGGTGCTGACACTCCCTCTCTGGGCAGTGGATGCAGCCATC 379

Qy    659 CAGTGGGTCTTTG 671
          |||||||||||||
Db    380 CAGTGGGTCTTTG 392


RESULT 12
BI653693
LOCUS       BI653693               871 bp    mRNA    linear   EST 12-SEP-2001
DEFINITION  603300354F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5340828 5',
            mRNA sequence.
ACCESSION   BI653693
VERSION     BI653693.1  GI:15567929
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11865  row: l  column: 13
            High quality sequence stop: 835.
FEATURES             Location/Qualifiers
     source          1. .871
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5340828"
                     /clone_lib="NIH_CGAP_Mam3"
                     /tissue_type="tumor, gross tissue"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert 2 kb. Library constructed by Life
                     Technologies, catalog #12017-018. Investigators providing
                     samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
                     for transgenic model: Xu et al., Nature Genetics 22, 37-43
                     (1999). Note: this is a NCI_CGAP Library."
BASE COUNT      164 a    274 c    221 g    212 t
ORIGIN

  Query Match             8.7%;  Score 162.8;  DB 10;  Length 871;
  Best Local Similarity   53.2%;  Pred. No. 9.2e-24;
  Matches  417;  Conservative    0;  Mismatches  357;  Indels   10;  Gaps    3;

Qy    575 ACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCG 634
          || || |||| ||||||| |||| || || |||||||  ||  |  | ||||  || ||
Db      1 ACGGATACCTACCTGCTCAACCTGGCCGTGGCAGACATCCTTTTCCTCCTGATTCTTCCC 60

Qy    635 CTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCA 694
           |||||||      ||  |||       ||| ||||||||     ||| || || | |
Db     61 TTCTGGGCCTACAGCGAAGCCAAGTCCTGGATCTTTGGCGTCTACCTGTGTAAGGGCATC 120

Qy    695 GGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTT 754
            || | |||  ||  | | ||||| |   ||    || |||||    ||||||||| ||
Db    121 TTTGGCATCTATAAGTTAAGCTTCTTCAGCGGGATGCTGCTGCTCCTATGCATCAGCATT 180

Qy    755 GACCGCTACCTGAACATAGTTCATGCC------ACCCAGCTCTACCGCCGGGGGCCCCCG 808
          ||||||||| |   ||| || || |||       | || | | |||||    |    |
Db    181 GACCGCTACGTAGCCATCGTCCAGGCCGTGTCGGCTCATCGCCACCGCGCCCGCGTGCTT 240
```

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Qy    809 GCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCA 868
Db    241 CTCATCAGCAAGCTGTCCTGTGTGGGCATCTGGATGCTGGCCCTCTTCCTCTCCATCCCG 300

Qy    869 GACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGC---CACCCACTGCCAA 925
Db    301 GAGCTGCTCTACAGCGGCCTCCAGAAGAACAGCGGCGAGGACACGCTGAGATGCTCACTG 360

Qy    926 TACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTT 985
Db    361 GTCAGTGCCCAAGTGGAGGCCTTGATCACCATCCAAGTGGCCCAGATGGTTTTTGGGTTC 420

Qy    986 CTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTT 1045
Db    421 CTAGTGCCTATGCTGGCTATGAGTTTCTGCTACCTCATTATCATCCGTACCTTGCTCCAG 480

Qy   1046 TCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTT 1105
Db    481 GCACGCAACTTTGAGCGGAACAAGGCCATCAAGGTGATCATTGCCGTGGTGGTAGTCTTC 540

Qy   1106 GCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGC 1165
Db    541 ATAGTCTTCCAGCTGCCCTACAATGGGGTGGTCCTGGCTCAGACGGTGGCCAACTTCAAC 600

Qy   1166 GCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCA 1225
Db    601 ATCACCAATAGCAGCTGCGAAACCAGCAAGCAGCTCAACATTGCCTATGACGTCACCTAC 660

Qy   1226 GGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAG 1285
Db    661 AGCCTGGCCTCCGTCCGCTGCTGCGTCAACCCTTTCTTGTATGCCTTCATCGGCGTCAAG 720

Qy   1286 TTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT-GGGCTGCCCCAACCAGAGAGGGCT 1344
Db    721 TTCCGCAGCGACCTCTTCAAGCTCTTCAAGGACTTGGGGCTGTCTCAGCCAGGAACGGCT 780

Qy   1345 CCAG 1348
Db    781 CCCG 784
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RESULT 13
AL523112
LOCUS AL523112 944 bp mRNA linear EST 13-FEB-2001
DEFINITION AL523112 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YB09 5 prime, mRNA sequence.
ACCESSION AL523112
VERSION AL523112.1 GI:12786605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 944)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .944
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC001YB09"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 106 a 357 c 301 g 174 t 6 others
ORIGIN

Query Match 8.6%; Score 161.2; DB 9; Length 944;
Best Local Similarity 51.3%; Pred. No. 2e-23;
Matches 463; Conservative 5; Mismatches 424; Indels 10; Gaps 4;

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Qy    436 GCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAG 495
Db     24 GCTTTGCTACAAGGCCGATGTCCAGGCCTTCAGCCGGGCCTTCCAACCCAGTGTCTCCCT 83

Qy    496 CCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCG 555
Db     84 GACCGTGGCTGCGCTGGGTCTGGCCGGCAATGGCCTGGTCCTGGCCACCCACCTGGCAGC 143

Qy    556 GCGGACAGCCCTGAGC-AGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGC 614
Db    144 CCGACGCGCAGCGCTCGCCCACCTCTGCCCACCTGCTCCAGCTGGCCCTGGCCGACCTCT 203

Qy    615 TGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCT 674
Db    204 TGCTGGCCCTGACTCTGCCCTTCGCGGCAGCAGGGGCTCTTCAGGGCTGGAGTCTGGGAA 263

Qy    675 CTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCC 734
Db    264 GTGCCACCTGCCGCACCATCTCTGGCCTCTACTCGGCCTCCTTCCACGCCGGCTTCCTCT 323

Qy    735 TGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTAC- 793
Db    324 TCCTGGCCTGTATCAGCGCCGACCGCTACGTGGCCATCGCGCGAVCTCCCAGCCGGGCCG 383

Qy    794 CGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTG 853
Db    384 CGGCCCTCCACTCCCGGCCGCGCACACTTGGTCTCCGTCATCGTGTGGCTGCTGTAACTG 443

Qy    854 CTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCAC------GACGAGCGCCTC 907
Db    444 CTCCTGGCGCTGCCTGCGCTGCTCTTCAGCCAGGATGGGCAGCGGGAAGGCCAACGACGC 503

Qy    908 AACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTG 967
Db    504 TGTCGCCTCAACTTCCCCGAGGGCCTCACGCAGACGGTGAAGGGGGCGAGCGCCGTGGCS 563

Qy    968 CAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATC 1027
Db    564 AGGGTGGCCCTGGGCTTCGCGCTGCCGCTGGGCGTCATGGTAGCCTGCTACGCGCTTCTG 623

Qy   1028 CTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTG 1087
Db    624 GGCCGCACGCTGCTGGCCGCCAGGGGGCCCGAGCGCCGGCGTGCGCYGCGCGTCGTGGTG 683

Qy   1088 GTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGAC 1147
Db    684 GCTCTGGTGGCGGCCTTCGTGGTGCTGCAGCYGCCCTACAGCCTCGCCCTGCTGCTGGAT 743

Qy   1148 ATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTG 1207
Db    744 ACTGCCGATCTACTGGCTGCGCGCGAGGGAGCTGCCCCTGCCAGCAAACGCAAGGATGTC 803

Qy   1208 GCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTAT 1267
Db    804 GCACTGCTGGTGACCAGCGGCTTGGCCCTCGCCCGCTGTGGCCTCAATCCCGTKCTCTAC 863

Qy   1268 GCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGC 1327
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Db    864 GC--TTTCTGGGCCTGCGCTTCCGCAGAACCTGCGGAGGCTGCTACGGGGTGGGAGCRGC 921

Qy   1328 CC 1329
          ||
Db    922 CC 923


RESULT 14
BI395190/c
LOCUS       BI395190                573 bp    mRNA    linear   EST 13-OCT-2001
DEFINITION  TUDPEc185 5'RACE cDNA Equus caballus cDNA clone TUDPEc185, mRNA
            sequence.
ACCESSION   BI395190
VERSION     BI395190.1  GI:16117704
KEYWORDS    EST.
SOURCE      horse.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 573)
  AUTHORS   Pascual,I., Dhar,A.K., Fan,Y., Paradis,M.R., Arruga,M.V. and
            Alcivar-Warren,A.
  TITLE     Isolation of expressed sequence tags from a Thoroughbred horse
            (Equus caballus) 5'RACE cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Alcivar-Warren, A.
            Department of Environmental and Population Health
            Tufts University School of Veterinary Medicine
            200 Westboro Road, North Grafton, MA 01536, USA
            Tel: (508) 839-7970
            Fax: (508) 839-7091
            Email: acacia.warren@tufts.edu
            The cDNA was isolated from blood cells (buffy coat) of a
            Thoroughbred septic foal
            PCR PRimers
            FORWARD: 5'-(CUA)4GGCCACGCGTCGACTAGTAC-3'
            BACKWARD: 5'-(CAU)4CTGTTTGAGCGGATGAAGGTGAA-3'
            Insert Length: 573   Std Error: 0.00
            Seq primer: M13 reverse.
FEATURES             Location/Qualifiers
     source          1. .573
                     /organism="Equus caballus"
                     /db_xref="taxon:9796"
                     /clone="TUDPEc185"
                     /clone_lib="5'RACE cDNA"
                     /tissue_type="Blood cells (buffy coat) from a septic
                     female"
                     /dev_stage="Foal"
                     /lab_host="E. coli DH5"
                     /note="Vector: pAMP1 (Gibco BRL); Obtained by 5'RACE
                     following the protocol of Gibco BRL. cDNA was  synthesized
                     using a gene-specific (IL1-ra) primer  (GSP1:
                     5'-CTGTTTGAGCGGATGAAGGT-3') from a genomic sequence. dCTP
                     was used to add a homopolymeric tail in the 3'end and the
                     tailed  cDNA was amplified by PCR using an anchor IL-1ra
                     gene-specific primer  (GSP2:
                     5'-CAUCAUCAUCAUCTGTTTGAGCGGATGAAGGTGAA-3') as the reverse
                     and  a Universal Anchor Primer (Gibco BRL) as the forward
                     primer. cDNA  was cloned through UDG cloning method."
BASE COUNT      138 a    135 c    200 g    100 t
ORIGIN

  Query Match             8.4%;  Score 158.4;  DB 10;  Length 573;
  Best Local Similarity   60.4%;  Pred. No. 7.4e-23;
  Matches  261;  Conservative    0;  Mismatches  171;  Indels    0;  Gaps    0;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          ||||  |    |  ||| ||||      |||  ||||| |||| || |||||  || ||||
Db    464 CTTCAAGGCCGTGTTCATGCCTATGGCCTATGGCCTCATCTTCCTTCTGGGTATGATGGG 405

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||  |  ||||   |   | |||  | | |  |||  | | |  | |  |||||| ||
Db    404 CAACATCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAAACACGCAACTCCACCGAGAC 345

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          |||||||  |||||||  ||   |  ||  |||    ||  |||||  ||  |   |||||  |    |
Db    344 CTTCCTGTTCCACCTGGCGTTGGCTGACCTCCTTCTGGTCCTCATCCTGCCCTTTGCTGT 285

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
          |   ||  |      ||     ||||||  |  |||  |  ||||||||||||    |      ||  ||
Db    284 GGCCGAGGGCTTTGTGGGCTGGGTCCTGGGCACCGGCCTCTGCAAAACTGTGATCGCTCT 225

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
             |||  ||||||||||||     |   |||  ||  ||||||||||||     | ||||||||
Db    224 GCACAAGATCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATTGCTGTGGACCGCTA 165

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  |||  ||  ||  ||  |||   ||||||||   | | ||    |  | |   | |
Db    164 CCTGGCCATTGTCCACTCCGTCCATACCTACCGCCACCGCCGCCTCCACTCCATCCACAT 105

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
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Db    104 CACCTGTATAACCATTTGGCTGGCGGGCCTCCTCTTCGCCTTGCCAGAGCTTCTCTTCGC 45

Qy    883 GTCGGCCCACCA 894
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RESULT 15
AL531903
LOCUS       AL531903                935 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  AL531903 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM003YH06 5
            prime, mRNA sequence.
ACCESSION   AL531903
VERSION     AL531903.1  GI:12795396
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector.  Library was normalized. Library was constructed
                     by Life Technologies.  Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      191 a    261 c    232 g    250 t      1 others
ORIGIN

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Qy    490 CTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCT 549
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Qy    550 GAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGA 609

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Qy    610 CACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTT 669

Db    319 CCTACTCTTTGCCCTGACCTTGCCCATCTGGGCCGCCTCCAAGGTGAATGGCTGGATTTT 378

Qy    670 TGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGC 729

Db    379 TGGCACATTCCTGTGCAAGGTGGTCTCACTCCTGAAGGAAGTCAACTTCTACAGTGGCAT 438

Qy    730 CCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCT 789

Db    439 CCTGCTGTTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGCAC 498

Qy    790 CTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTG 849

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Qy    850 CCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACC------ACGACGAGCG 903

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Qy   1144 GGACATCCTCATG 1156

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Search completed: November 2, 2002, 06:28:04
Job time : 1694 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 04:12:07 ; Search time 2851 Seconds
(without alignments)
14236.082 Million cell updates/sec

Title: US-09-101-518A-1
Perfect score: 1876
Sequence: 1 cctgaagggagagcagggag.....atcgtcaggaaaaaaaaaaa 1876

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1874.4	99.9	1876	1	PCT-US96-00499-1	Sequence 1, Appli
2	1874.4	99.9	1876	1	PCT-US96-00499A-1	Sequence 1, Appli
3	1874.4	99.9	1876	15	US-09-101-518-1	Sequence 1, Appli
4	1873.2	99.9	1877	1	PCT-US00-26524B-2115	Sequence 2115, Ap
c 5	1839.2	98.0	6604	64	US-60-258-273-3	Sequence 3, Appli
6	1548.4	82.5	1670	14	US-09-023-655-980	Sequence 980, App
7	1548.4	82.5	1670	33	US-09-880-107-3833	Sequence 3833, Ap
8	1541.6	82.2	1670	24	US-09-624-594-1	Sequence 1, Appli
9	1541.6	82.2	1670	24	US-09-633-541-1	Sequence 1, Appli
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11	1541.6	82.2	1670	26	US-09-663-799-1	Sequence 1, Appli
12	1530.6	81.6	1626	64	US-60-258-273-211	Sequence 211, App
13	1293	68.9	1293	14	US-09-016-434-1052	Sequence 1052, Ap
14	1293	68.9	1293	36	US-09-960-706-962	Sequence 962, App
15	1097	58.5	1107	15	US-09-170-496-19	Sequence 19, Appl
16	1097	58.5	1107	15	US-09-170-496C-19	Sequence 19, Appl
17	1097	58.5	1107	15	US-09-170-496D-19	Sequence 19, Appl
18	1095.4	58.4	1107	15	US-09-170-496C-173	Sequence 173, App
19	1095.4	58.4	1107	15	US-09-170-496D-173	Sequence 173, App
20	849.2	45.3	1608	75	US-60-360-207-302	Sequence 302, App
21	844.4	45.0	1620	14	US-09-010-701C-21	Sequence 21, Appl
22	840.2	44.8	2914	60	US-60-212-655-911	Sequence 911, App
23	775	41.3	814	60	US-60-213-169-650	Sequence 650, App
24	775	41.3	814	60	US-60-213-170-650	Sequence 650, App
25	750.2	40.0	965	60	US-60-213-844-16	Sequence 16, Appl
26	729	38.9	1024	27	US-09-699-011A-485	Sequence 485, App
27	695	37.0	2836	61	US-60-229-515-1618	Sequence 1618, Ap
c 28	615	32.8	615	37	US-10-029-386-25025	Sequence 25025, A
29	613	32.7	625	58	US-60-192-587-129	Sequence 129, App
30	613	32.7	625	58	US-60-192-587-748	Sequence 748, App
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	32	613	32.7	625	58	US-60-194-091-142	Sequence 142, App
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ALIGNMENTS

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;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;    TITLE OF INVENTION:  HSATU68
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00499
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferraro, Gregory D
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-474
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
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;    SEQUENCE CHARACTERISTICS:
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;      TOPOLOGY:  linear
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;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  173..1417
PCT-US96-00499-1

  Query Match             99.9%;  Score 1874.4;  DB 1;  Length 1876;
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  Matches 1875;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
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Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAA 1876
          ||||||||||||||||
Db   1861 TCAGGAAAAAAAAAAA 1876


RESULT 2
PCT-US96-00499A-1
; Sequence 1, Application PC/TUS9600499A
;  GENERAL INFORMATION:
;    APPLICANT:  LI, Yi
;    TITLE OF INVENTION:  Human G-Protein Chemokine Receptor
;    TITLE OF INVENTION:  HSATU68
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain, Gilfillan, Cecchi,
;      ADDRESSEE:  Stewart & Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  07068-1739
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/00499A
;      FILING DATE:  11 JAN 1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MULLINS, J.G.
;      REGISTRATION NUMBER:  33,073
;      REFERENCE/DOCKET NUMBER:  325800-474
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744.
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1876 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  173..1417
PCT-US96-00499A-1

  Query Match             99.9%;  Score 1874.4;  DB 1;  Length 1876;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1875;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120

Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300

Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
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Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140

Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAAA 1876
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Db   1861 TCAGGAAAAAAAAAAAA 1876
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RESULT 3
US-09-101-518-1
; Sequence 1, Application US/09101518
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
; FILE REFERENCE: PF218PCT.US
; CURRENT APPLICATION NUMBER: US/09/101,518
; CURRENT FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: PCT/US96/00499
; PRIOR FILING DATE: 1996-01-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1876
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)..(1420)
US-09-101-518-1

Query Match 99.9%; Score 1874.4; DB 15; Length 1876;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1875; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120

Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300

Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCAGCCCTCAACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
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Db    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720

Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140

Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
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Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAA 1876
          ||||||||||||||||
Db   1861 TCAGGAAAAAAAAAAA 1876
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RESULT 4
PCT-US00-26524B-2115
; Sequence 2115, Application PC/TUS0026524B
; GENERAL INFORMATION:
; APPLICANT: Birse et. al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005PCT
; CURRENT APPLICATION NUMBER: PCT/US00/26524B
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2115
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-26524B-2115

Query Match 99.9%; Score 1873.2; DB 1; Length 1877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1872; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120

Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300

Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAMTC 420

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
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Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
          ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720

Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140

Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
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Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAAA 1876
          |||||||||||||||||
Db   1861 TCAGGAAAAAAAAAAAA 1876
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RESULT 5
US-60-258-273-3/c
; Sequence 3, Application US/60258273
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
;  TITLE OF INVENTION:  HORMONE RECEPTOR PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001042-PROV
;  CURRENT APPLICATION NUMBER: US/60/258,273
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 6604
;   TYPE: DNA
;   ORGANISM: Human
US-60-258-273-3

  Query Match             98.0%;  Score 1839.2;  DB 64;  Length 6604;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1863;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   3872 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGGCAGAGAGGGCTCTGGGCACTGGAGG 3813

Qy     61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3812 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 3753

Qy    121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   3752 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGGCTGAGCGGATGGAGTT 3693

Qy    181 GAGGAAGTACGG-CCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTA 239
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3692 GAGGAAGTACGGTCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTA 3633

Qy    240 AATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCC 299
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3632 AATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCC 3573

Qy    300 CTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGG 359
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3572 CTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGG 3513

Qy    360 TTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACT 419
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Db   3512 TTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACT 3453

Qy    420 CGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCC 479
Db   3452 CGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCC 3393

Qy    480 TGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAG 539
Db   3392 TGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAG 3333

Qy    540 CCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAG 599
Db   3332 CCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAG 3273

Qy    600 CTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCC 659
Db   3272 CTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCC 3213

Qy    660 AGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCT 719
Db   3212 AGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCT 3153

Qy    720 ACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATG 779
Db   3152 ACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATG 3093

Qy    780 CCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCT 839
Db   3092 CCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCT 3033

Qy    840 GGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACG 899
Db   3032 GGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACG 2973

Qy    900 AGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGC 959
Db   2972 AGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGC 2913

Qy    960 GGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATG 1019
Db   2912 GGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATG 2853

Qy   1020 CCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGC 1079
Db   2852 CCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGC 2793

Qy   1080 TGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGC 1139
Db   2792 TGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGC 2733

Qy   1140 TGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGG 1199
Db   2732 TGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGG 2673

Qy   1200 TAG-ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCG 1258
Db   2672 TAGTACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCG 2613

Qy   1259 CTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGC 1318
Db   2612 CTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGC 2553

Qy   1319 CTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCA 1378
Db   2552 CTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCA 2493

Qy   1379 TCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCC 1438
Db   2492 TCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCC 2433

Qy   1439 CCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCT 1498
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Db   2432 CCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCT 2373

Qy   1499 GGCTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTC 1558
Db   2372 GGCTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTC 2313

Qy   1559 CCGGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGC 1618
Db   2312 CCGGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGC 2253

Qy   1619 CCCATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTA 1678
Db   2252 CCCATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTA 2193

Qy   1679 AAACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCAT 1738
Db   2192 AAACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCAT 2133

Qy   1739 GAAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCT 1798
Db   2132 GAAGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCT 2073

Qy   1799 ATATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGAT 1858
Db   2072 ATATTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGAT 2013

Qy   1859 CGTCAGGA 1866
Db   2012 CGTCAGGA 2005
```

RESULT 6
US-09-023-655-980
; Sequence 980, Application US/09023655
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 980:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1670 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g1552845
US-09-023-655-980

  Query Match             82.5%;  Score 1548.4;  DB 14;  Length 1670;
  Best Local Similarity   99.0%;  Pred. No. 1.1e-313;
  Matches 1558;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
           ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db      58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy     363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy     423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGAAAAAAAAAAAA 1876
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Db    1618 AGGACCAAAAAAAA 1631


RESULT 7
US-09-880-107-3833
; Sequence 3833, Application US/09880107
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3833
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. X95876
US-09-880-107-3833

  Query Match             82.5%;  Score 1548.4;  DB 33;  Length 1670;
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  Best Local Similarity   99.0%;  Pred. No. 1.1e-313;
  Matches 1558;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db      58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy     363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Db     118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy     423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
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Db     238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
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Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
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Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db     958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGAAAAAAAAAAAA 1876
           ||||  ||||||||
Db    1618 AGGACCAAAAAAAAA 1631
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RESULT 8
US-09-624-594-1
; Sequence 1, Application US/09624594
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/624,594
; FILING DATE: 25-JUL-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,838
; FILING DATE: 10-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: TKI96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540

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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1670 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  69..1172
US-09-624-594-1

  Query Match             82.2%;  Score 1541.6;  DB 24;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-312;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db      58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy     363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Qy     423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
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Db     178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
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Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
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Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
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Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
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Db    1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
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Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGA 1866
           ||||
Db    1618 AGGA 1621


RESULT 9
US-09-633-541-1
; Sequence 1, Application US/09633541
;  GENERAL INFORMATION:
;    APPLICANT:  Loetscher, Marcel
;    APPLICANT:  Moser, Bernhard
;    TITLE OF INVENTION:  IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;    TITLE OF INVENTION:  NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/09/633,541
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/709,838
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brook Esq., David E.
;       REGISTRATION NUMBER:  22,592
;       REFERENCE/DOCKET NUMBER:  TKI96-01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 861-6240
;       TELEFAX:  (617) 861-9540
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1670 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  69..1172
US-09-633-541-1

  Query Match             82.2%;  Score 1541.6;  DB 24;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-312;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db      58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy     363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Db     118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy     423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
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Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
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Db     718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db     958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGA 1866
           ||||
Db    1618 AGGA 1621


RESULT 10
US-09-663-702-1
; Sequence 1, Application US/09663702
;   GENERAL INFORMATION:
;       APPLICANT: Loetscher, Marcel
;                  Moser, Bernhard
;                  Qin, Shixin
;                  Mackay, Charles R.
;       TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
```

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;                          ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;            STREET: Two Militia Drive
;            CITY: Lexington
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02173
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/663,702
;            FILING DATE: 15-Sep-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/829,839
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Brook Esq., David E.
;            REGISTRATION NUMBER: 22,592
;            REFERENCE/DOCKET NUMBER: TKI96-01A
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617) 861-6240
;            TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1670 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  69..1172
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-702-1

  Query Match             82.2%;  Score 1541.6;  DB 26;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-312;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||    |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
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Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
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Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
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Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
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Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
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Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
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Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
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Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
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Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGA 1866
          ||||
Db   1618 AGGA 1621


RESULT 11
US-09-663-799-1
; Sequence 1, Application US/09663799
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/663,799
;             FILING DATE: 15-Sep-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/709,838
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1670 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  69..1172
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-663-799-1

  Query Match            82.2%;  Score 1541.6;  DB 26;  Length 1670;
  Best Local Similarity  99.1%;  Pred. No. 3.6e-312;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377
```

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Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGA 1866
          ||||
Db   1618 AGGA 1621


RESULT 12
US-60-258-273-211
; Sequence 211, Application US/60258273
; GENERAL INFORMATION:
;  APPLICANT: Beasley, Ellen
;  TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR
;  TITLE OF INVENTION:  PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR
;  TITLE OF INVENTION:  HORMONE RECEPTOR PROTEINS, AND USES THEREOF
;  FILE REFERENCE: CL001042-PROV
;  CURRENT APPLICATION NUMBER: US/60/258,273
;  CURRENT FILING DATE:  2000-12-27
;  NUMBER OF SEQ ID NOS: 312
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 211
;   LENGTH: 1626
;   TYPE: DNA
;   ORGANISM: Human
US-60-258-273-211

  Query Match             81.6%;  Score 1530.6;  DB 64;  Length 1626;
  Best Local Similarity   99.0%;  Pred. No. 7.1e-310;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    1;  Gaps    1;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||||||
Db     59 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 118

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    119 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 178

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    179 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 238

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    239 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 298

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    299 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 358

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 418

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 478

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 538

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 598

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 658

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 718

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 778

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 838

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 898

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 958

Qy   1203 -ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTG 1261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 TACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTG 1018

Qy   1262 CTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTG 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 CTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTG 1078

Qy   1322 GGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCC 1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 GGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCC 1138

Qy   1382 TGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCT 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 TGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCT 1198

Qy   1442 TTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGC 1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 TTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGC 1258

Qy   1502 TCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCG 1561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1259 TCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCG 1318

Qy   1562 GGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCC 1621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1319 GGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCC 1378

Qy   1622 ATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAA 1681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1379 ATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAA 1438

Qy   1682 CTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAA 1741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1439 CTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAA 1498

Qy   1742 GCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATA 1801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1499 GCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATA 1558

Qy   1802 TTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGT 1861
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1559 TTTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGT 1618

Qy   1862 CAGGA 1866
          |||||
Db   1619 CAGGA 1623


RESULT 13
US-09-016-434-1052
; Sequence 1052, Application US/09016434
;  GENERAL INFORMATION:
;     APPLICANT:  Janice Au-Young
;     APPLICANT:  Jeffrey J. Seilhamer
;     TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;     TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;     NUMBER OF SEQUENCES:  1490
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;       STREET:  3174 PORTER DRIVE
;       CITY:  PALO ALTO
;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/016,434
;       FILING DATE:  HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Zeller, Karen J.
;       REGISTRATION NUMBER:  37,071
;       REFERENCE/DOCKET NUMBER:  PA-0002 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 855-0555
;       TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1052:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1293 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  GENBANK
;       CLONE:  g1002740
US-09-016-434-1052

  Query Match             68.9%;  Score 1293;  DB 14;  Length 1293;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-260;
  Matches 1293;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    218 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy    278 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy    338 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy    398 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy    458 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy    518 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy    578 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy    638 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy    698 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy    758 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy    818 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy    878 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy    938 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy    998 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy   1058 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy   1118 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 1177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy   1178 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy   1238 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy   1298 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy   1358 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

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Db   1201 TGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTC 1260

Qy   1478 CTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAA 1510
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RESULT 14
US-09-960-706-962
; Sequence 962, Application US/09960706
; GENERAL INFORMATION:
;  APPLICANT: Munger, William E.
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
;  TITLE OF INVENTION:  Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-01US
;  CURRENT APPLICATION NUMBER: US/09/960,706
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 60/223,323
;  PRIOR FILING DATE: 2000-08-07
;  PRIOR APPLICATION NUMBER: 09/873,319
;  PRIOR FILING DATE: 2001-06-05
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
;   LENGTH: 1293
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U32674
US-09-960-706-962

  Query Match             68.9%;  Score 1293;  DB 36;  Length 1293;
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Qy    278 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 337
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Db     61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy    338 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 397
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Qy    398 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 457
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Qy    458 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 517
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Qy    638 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 697
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Qy    698 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 757
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Qy    758 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 817
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Db    721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy    998 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 1057
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Qy   1058 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 1117
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Qy   1118 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 1177
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Qy   1178 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1237
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Db    961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy   1238 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1297
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Db   1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

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RESULT 15
US-09-170-496-19
; Sequence 19, Application US/09170496
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupl
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-170-496-19

  Query Match             58.5%;  Score 1097;  DB 15;  Length 1107;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-219;
  Matches 1097;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
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Job time : 2887 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 2, 2002, 04:08:52 ; Search time 429 Seconds
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Title: US-09-101-518A-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1873.2	99.9	1877	12	US-10-106-698-2125	Sequence 2125, Ap
3	1548.4	82.5	1670	2	PCT-US02-18947-620	Sequence 620, App
4	1548.4	82.5	1670	2	PCT-US02-25766-2790	Sequence 2790, Ap
5	1548.4	82.5	1670	12	US-10-172-118-620	Sequence 620, App
6	1541.6	82.2	1670	13	US-10-251-686-1	Sequence 1, Appli
7	1293	68.9	1293	2	PCT-US02-30182-962	Sequence 962, App
8	1097	58.5	1107	11	US-10-251-385-19	Sequence 19, Appl
9	1095.4	58.4	1107	11	US-10-251-385-173	Sequence 173, App
10	240	12.8	1119	13	US-10-035-832-1414	Sequence 1414, Ap
11	240	12.8	2824	13	US-10-035-832-1413	Sequence 1413, Ap
12	240	12.8	32404	13	US-10-035-832-1412	Sequence 1412, Ap
13	238.4	12.7	1119	11	US-10-251-385-65	Sequence 65, Appl
14	238.4	12.7	1119	11	US-10-251-385-199	Sequence 199, App
15	238.4	12.7	2818	9	US-09-442-384B-424	Sequence 424, App
16	216.6	11.5	1137	11	US-10-251-385-73	Sequence 73, Appl
17	216.6	11.5	1137	13	US-10-035-832-976	Sequence 976, App
18	216.6	11.5	2139	2	PCT-US02-18947-678	Sequence 678, App
19	216.6	11.5	2139	12	US-10-172-118-678	Sequence 678, App
20	216.6	11.5	2139	13	US-10-035-832-975	Sequence 975, App
21	216.6	11.5	2172	13	US-10-247-671-43	Sequence 43, Appl
22	216.6	11.5	2192	12	US-10-143-982-64	Sequence 64, Appl
23	216.6	11.5	31670	13	US-10-035-832-974	Sequence 974, App
24	215	11.5	1137	11	US-10-251-385-203	Sequence 203, App
25	206.6	11.0	2207	12	US-10-143-982-159	Sequence 159, App
26	206.6	11.0	2207	13	US-10-211-364-613	Sequence 613, App
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33	206.6	11.0	2207	13	US-10-219-917-194	Sequence 194, App
34	203.2	10.8	1777	13	US-10-252-157-227	Sequence 227, App
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44	198.8	10.6	1137	13	US-10-035-832-973	Sequence 973, App
45	198.8	10.6	2072	13	US-10-035-832-972	Sequence 972, App

ALIGNMENTS

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US-09-101-518A-1
; Sequence 1, Application US/09101518A
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  TITLE OF INVENTION: Human G-Protein Chemokine Receptor HSATU68
;  FILE REFERENCE: PF218US
;  CURRENT APPLICATION NUMBER: US/09/101,518A
;  CURRENT FILING DATE:  2002-03-18
;  PRIOR APPLICATION NUMBER: PCT/US96/00499
;  PRIOR FILING DATE: 1996-01-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1876
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (173)..(1420)
;   OTHER INFORMATION:
US-09-101-518A-1

  Query Match             100.0%;  Score 1876;  DB 9;  Length 1876;
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  Matches 1876;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
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Db    301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420

Qy    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720

Qy    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy   1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200

Qy   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260
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Db   1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
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Db   1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
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Db   1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
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Db   1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860

Qy   1861 TCAGGAAAAAAAAAAA 1876
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RESULT 2
US-10-106-698-2125
; Sequence 2125, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2125
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-2125

Query Match 99.9%; Score 1873.2; DB 12; Length 1877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1872; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
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Db      1 CCTGAAGGGAGAGCAGGGAGAGAGAGGACAGTGGCCAGAGAGGGCTCTGGGCACTGGAGG 60
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Qy      61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120
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Db      61 GACGCTCTTCTTCCTGCCCAGGGGTCCCTGGGCCGATGGGATCACGCAGAAGAATGCGAG 120

Qy     121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180
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Db     121 AGAAGCAGCCTTTGAGAAGGGAAGTCACTATCCCAGAGCCCAGACTGAGCGGATGGAGTT 180

Qy     181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240
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Db     181 GAGGAAGTACGGCCCTGGAAGACTGGCGGGGACAGTTATAGGAGGAGCTGCTCAGAGTAA 240

Qy     241 ATCACAGACTAAATCAGACTCAATCACAAAAGAGTTCCTGCCAGGCCTTTACACAGCCCC 300
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Qy     301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGT 360

Qy     361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTC 420
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Db     361 TGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGAMTC 420

Qy     421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480
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Db     421 GTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCT 480

Qy     481 GCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540
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Db     481 GCCAGCCCTCWACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGC 540

Qy     541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600
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Db     541 CGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGC 600

Qy     601 TGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660
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Db     601 TGTAGCAGACACRCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCA 660

Qy     661 GTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTA 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780
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Db     721 CGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGC 780

Qy     781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840
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Db     781 CACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTG 840

Qy     841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900
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Db     841 GGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGA 900

Qy     901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960
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Db     901 GCGCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCG 960

Qy     961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGC 1020

Qy    1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080
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Db    1021 CCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCT 1080

Qy    1081 GGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCT 1140
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Qy    1141 GGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGT 1200
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Db    1201 AGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCT 1260

Qy    1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCT 1320

Qy    1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATC 1380

Qy    1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCC 1440

Qy    1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500
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Db    1441 TTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGG 1500

Qy    1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560
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Db    1501 CTCTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCC 1560

Qy    1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGGAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCC 1620

Qy    1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 CATCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAA 1680

Qy    1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740
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Db    1681 ACTTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGA 1740

Qy    1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 AGCCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTAT 1800

Qy    1801 ATTTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCG 1860
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Qy    1861 TCAGGAAAAAAAAAAA 1876
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Db    1861 TCAGGAAAAAAAAAAA 1876
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RESULT 3
PCT-US02-18947-620
; Sequence 620, Application PC/TUS0218947
; GENERAL INFORMATION:
;  APPLICANT: Rosetta Inpharmatics
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-228
;  CURRENT APPLICATION NUMBER: PCT/US02/18947
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 620
;   LENGTH: 1670
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: NM_001504
;   DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-620
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  Query Match            82.5%;  Score 1548.4;  DB 2;  Length 1670;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
           ||  |||   |  |  |    ||||||||||||||||||||||||||||||||||||||
Db      58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy     363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
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Db     118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy     423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
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Db     178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy     483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy     543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy     603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy     663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db     418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy     723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
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Db     478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy     783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
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Db     538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy     843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
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Db     598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy     903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db     658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy     963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy    1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy    1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
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Db     838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy    1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy    1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy    1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy    1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy    1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy    1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy    1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy    1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy    1623 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy    1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy    1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy    1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy    1863 AGGAAAAAAAAAAAA 1876
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Db    1618 AGGACCAAAAAAAAA 1631
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RESULT 4
PCT-US02-25766-2790
; Sequence 2790, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/311,837
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2790
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X95876
PCT-US02-25766-2790

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  Query Match            82.5%;  Score 1548.4;  DB 2;  Length 1670;
  Best Local Similarity  99.0%;  Pred. No. 0;
  Matches 1558;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy     303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
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Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
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Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGAAAAAAAAAAAA 1876
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Db   1618 AGGACCAAAAAAAA 1631
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RESULT 5
US-10-172-118-620
; Sequence 620, Application US/10172118
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 620
; LENGTH: 1670
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001504
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-620

Query Match 82.5%; Score 1548.4; DB 12; Length 1670;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
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Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177
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Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
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Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
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Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
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Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
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Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
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Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
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Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
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Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
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Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
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Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
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Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257
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Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377
.
Qy   1623 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCCATGAAG 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGAAAAAAAAAAA 1876
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Db   1618 AGGACCAAAAAAAA 1631
```

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RESULT 6
US-10-251-686-1
; Sequence 1, Application US/10251686
;   GENERAL INFORMATION:
;        APPLICANT: Loetscher, Marcel
;                   Moser, Bernhard
;                   Qin, Shixin
;                   Mackay, Charles R.
;        TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
;                            ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;             STREET: Two Militia Drive
;             CITY: Lexington
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02173
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/251,686
;             FILING DATE: 20-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/829,839
;             FILING DATE: 31-MAR-1997
;             APPLICATION NUMBER: US 08/709,838
;             FILING DATE: 10-SEP-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Brook Esq., David E.
;             REGISTRATION NUMBER: 22,592
;             REFERENCE/DOCKET NUMBER: TKI96-01A
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 861-6240
;             TELEFAX: (617) 861-9540
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1670 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
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;            TOPOLOGY: unknown
;          FEATURE:
;               NAME/KEY:  CDS
;               LOCATION:  69..1172
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-251-686-1

  Query Match             82.2%;  Score 1541.6;  DB 13;  Length 1670;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1550;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy    303 CCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 362
          ||  |||   |  |  |    |||||||||||||||||||||||||||||||||||||||
Db     58 CCAGCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTG 117

Qy    363 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGT 177

Qy    423 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 GCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGC 237

Qy    483 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 542
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 CAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCG 297

Qy    543 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTG 357

Qy    603 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 TAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGT 417

Qy    663 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 GGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACG 477

Qy    723 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 CAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCA 537

Qy    783 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    538 CCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGG 597

Qy    843 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    598 GGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGC 657

Qy    903 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    658 GCCTCAACGCCACCCACTGCCAATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGG 717

Qy    963 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 1022
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    718 TGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCC 777

Qy   1023 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 1082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    778 ACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGG 837

Qy   1083 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    838 TGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGG 897

Qy   1143 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 1202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    898 TGGACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAG 957

Qy   1203 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    958 ACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGC 1017

Qy   1263 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1018 TCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGG 1077

Qy   1323 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1078 GCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCT 1137

Qy   1383 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1138 GGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCCGGAATCCGGGCTCCCCTT 1197

Qy   1443 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1198 TCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCT 1257

Qy   1503 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1258 CTCCCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACCACCAGGTCTCCCGG 1317

Qy   1563 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1318 GAAGCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCA 1377

Qy   1623 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1378 TCCTGCCGCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAAACTAAAAC 1437

Qy   1683 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1438 TTCATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAG 1497

Qy   1743 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1498 CCACAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATAT 1557

Qy   1803 TTGGTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1862
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1558 TTGCTCTTTTATTTTTATGTCTAAAATCCTGCTTAAAACTTTTCAATAAACAAGATCGTC 1617

Qy   1863 AGGA 1866
          ||||
Db   1618 AGGA 1621


RESULT 7
PCT-US02-30182-962
; Sequence 962, Application PC/TUS0230182
; GENERAL INFORMATION:
;  APPLICANT: Gene Logic, Inc.
;  APPLICANT:  Munger, William E.
;  APPLICANT:  Kulkarni, Prakash
;  APPLICANT:  Getzenberg, Robert H.
;  APPLICANT:  Waga, Iwao
;  APPLICANT:  Yamamoto, Jun
;  TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperp
;  TITLE OF INVENTION:  Gene Expression Profiles
;  FILE REFERENCE: 44921-5029-01-WO
;  CURRENT APPLICATION NUMBER: PCT/US02/30182
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: 09/960,706
;  PRIOR FILING DATE: 2001-09-24
;  NUMBER OF SEQ ID NOS: 1124
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 962
;   LENGTH: 1293
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. U32674
PCT-US02-30182-962
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  Query Match             68.9%;  Score 1293;  DB 2;  Length 1293;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-267;
  Matches 1293;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     218 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATAGGAGGAGCTGCTCAGAGTAAATCACAGACTAAATCAGACTCAATCACAAAAGAGTTC 60

Qy     278 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCCAGGCCTTTACACAGCCCCTTCCTCCCCGTTCCCGCCCTCACAGGTGAGTGACCAC 120

Qy     338 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCAGCTCTTCCTATGAC 180

Qy     398 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCCCACAGGACTTCAGC 240

Qy     458 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTG 300

Qy     518 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACC 360

Qy     578 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTC 420

Qy     638 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGT 480

Qy     698 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGAC 540

Qy     758 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTG 600

Qy     818 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATC 660

Qy     878 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACAACTTCCCA 720

Qy     938 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCTGCTGCCCCTG 780

Qy     998 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 1057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAG 840

Qy    1058 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 1117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGG 900

Qy    1118 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 1177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGGCGCTTTGGCCCGC 960

Qy    1178 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTAC 1020

Qy    1238 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGG 1080

Qy    1298 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGCTCCAGAGGCAGCCA 1140

Qy    1358 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCTCCTACTCGGGCTTG 1200

Qy    1418 TGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTC 1477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TGAGGCCGGAATCCGGGCTCCCCTTTCGCCCACAGTCTGACTTCCCCGCATTCCAGGCTC 1260

Qy    1478 CTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAA 1510
           ||||||||||||||||||||||||||||||||
Db    1261 CTCCCTCCCTCTGCCGGCTCTGGCTCTCCCCAA 1293


RESULT 8
US-10-251-385-19
; Sequence 19, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-251-385-19

  Query Match             58.5%;  Score 1097;  DB 11;  Length 1107;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-225;
  Matches 1097;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      11 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 70

Qy     384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      71 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 130

Qy     444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 190

Qy     504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     191 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 250

Qy     564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     251 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 310

Qy     624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     311 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 370

Qy     684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 430

Qy      744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      431 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 490

Qy      804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 550

Qy      864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      551 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 610

Qy      924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      611 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 670

Qy      984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      671 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 730

Qy     1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      731 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 790

Qy     1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      791 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 850

Qy     1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      851 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 910

Qy     1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      911 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 970

Qy     1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      971 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1030

Qy     1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1031 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1090

Qy     1404 CCTACTCGGGCTTGTGA 1420
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Db     1091 CCTACTCGGGCTTGTGA 1107
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RESULT 9
US-10-251-385-173
; Sequence 173, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
;   LENGTH: 1107
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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US-10-251-385-173

  Query Match             58.4%;  Score 1095.4;  DB 11;  Length 1107;
  Best Local Similarity   99.9%;  Pred. No. 3e-225;
  Matches 1096;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      324 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 383
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       11 AGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCGCCCTCCTGGAGAACTTCA 70

Qy      384 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 443
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       71 GCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCTGTACCTCCCCGCCCTGCC 130

Qy      444 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 503
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      131 CACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCT 190

Qy      504 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 563
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      191 TTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAG 250

Qy      564 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 623
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      251 CCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGC 310

Qy      624 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 683
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      311 TGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCT 370

Qy      684 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 743
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      371 GCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCT 430

Qy      744 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 803
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      431 GCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGC 490

Qy      804 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 863
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      491 CCCCGGCCCGCGTGACCCTCACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCC 550

Qy      864 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 923
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      551 TCCCAGACTTCATCTTCCTGTCGGCCCACCACGACGAGCGCCTCAACGCCACCCACTGCC 610

Qy      924 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 983
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      611 AATACAACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCT 670

Qy      984 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 1043
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      671 TTCTGCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTGCTGG 730

Qy     1044 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 1103
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      731 TTTCCAGGGGCCAGCGGCGCCTGCGGGCCAAGCGGCTGGTGGTGGTGGTCGTGGTGGCCT 790

Qy     1104 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 1163
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      791 TTGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGG 850

Qy     1164 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 1223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      851 GCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCT 910

Qy     1224 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 1283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      911 CAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCA 970

Qy     1284 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      971 AGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACCAGAGAGGGC 1030
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Qy   1344 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1031 TCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTCATCCTGGTCTGAGACCTCAGAGGCCT 1090

Qy   1404 CCTACTCGGGCTTGTGA 1420
          |||||||||||||||||
Db   1091 CCTACTCGGGCTTGTGA 1107


RESULT 10
US-10-035-832-1414
; Sequence 1414, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1414
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-035-832-1414

  Query Match             12.8%;  Score 240;  DB 13;  Length 1119;
  Best Local Similarity   57.0%;  Pred. No. 9.4e-42;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db    144 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 203

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db    204 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 263

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   |||||||  | |   ||||  |    |
Db    264 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 323

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
            |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db    324 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 383

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
             |||  ||||||||||     |   ||| || ||||||||||||  | | ||||||||
Db    384 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 443

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || |||  |||   ||||||||  | | ||    |  | |   | |
Db    444 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 503

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||    | |  |||||  | |  || | ||  | ||| | |||||  |  |||||
Db    504 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 563

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
              | |  ||| | | | | |  |||| |          ||||  || |||| | ||
Db    564 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 623

Qy    931 CTTCCCACA---GGTGGGCCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |   | | |     |    ||  | ||  | |  ||||| || || ||
Db    624 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 683

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
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          ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db    684 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 743

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
               || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db    744 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 803

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
             |||||||||| | ||||| ||| | ||  |  |  ||||||  |||   |   |||
Db    804 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 863

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
             ||  ||| |   | |||     |   |  ||     |   ||||||||   |  |
Db    864 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 923

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
             |||||||      ||||||||||||||||  |||||||  | || |  || || ||
Db    924 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 983

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||        ||| |  ||| ||   |   ||||||||  ||  ||
Db    984 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1033


RESULT 11
US-10-035-832-1413
; Sequence 1413, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1413
;   LENGTH: 2824
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-035-832-1413

  Query Match             12.8%;  Score 240;  DB 13;  Length 2824;
  Best Local Similarity   57.0%;  Pred. No. 1.1e-41;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db    228 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 287

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | ||| | | |  |||    | |  ||   ||| || ||
Db    288 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 347

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db    348 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 407

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
            |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db    408 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 467

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
             |||  ||||||||||     |   ||| || ||||||||||||  | | ||||||||
Db    468 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 527

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || |||  |||   ||||||||  | | ||    |  | |   | |
Db    528 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 587
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Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||    | |  |||||  | |  || | ||  | ||| | |||||   |  |||||
Db    588 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 647

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
            | |  ||| | | | | |  |||| |           ||||  || |||| | ||
Db    648 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 707

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |  | | |     |    ||  | ||  | |  |||||  || || ||
Db    708 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 767

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db    768 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 827

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
            || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db    828 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 887

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
            ||||||||||  | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db    888 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 947

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
           ||  ||| |   | |||    |   |  ||    |   ||||||||   | |
Db    948 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1007

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
             |||||||      ||||||||||||||||  |||||||  | || |  || || ||
Db   1008 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||        ||| |  ||| ||   |   ||||||||  ||  ||
Db   1068 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 1117


RESULT 12
US-10-035-832-1412
; Sequence 1412, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT:  Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1412
;   LENGTH: 32404
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (384)..(403)
;   OTHER INFORMATION: "n" at positions 384 thru 403 can be any base
US-10-035-832-1412

  Query Match           12.8%;  Score 240;  DB 13;  Length 32404;
  Best Local Similarity   57.0%;  Pred. No. 1.9e-41;
  Matches  507;  Conservative    0;  Mismatches  365;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |    |||||||||| |||| || |||||  || | ||
Db  19830 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 19889

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          |||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db  19890 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 19949

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db  19950 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 20009

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
            |  || |   | ||    |||||| | ||  |   ||||||||||   |    ||||||
Db  20010 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 20069

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
            |||  ||||||||||||    |   ||| || ||||||||||||  | | ||||||||
Db  20070 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 20129

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || ||| |||   |||||||||   | | ||    | | |   | |
Db  20130 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 20189

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||   | |  |||||  | |  || | ||  | ||| | |||||  |  |||||
Db  20190 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 20249

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC----------CACCCACTGCCAATACAA 930
            | |  ||| | | | | |  |||| |           ||||  || |||| | ||
Db  20250 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 20309

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |  | | |     |    ||  | ||  | |  |||||  || || ||
Db  20310 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 20369

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          ||||||| ||||||| |||| ||  ||||| |      |  ||  |  | ||   | ||
Db  20370 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 20429

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
            || |||  | ||| | |  |||  |  || |||   |  ||||         |||
Db  20430 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 20489

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
            ||||||||||  | ||||| ||| | ||  |  |  |||||| |||   |   |||
Db  20490 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 20549

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
           ||  ||| |   | |||    |   |  ||    |   ||||||||   | |
Db  20550 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 20609

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
             |||||||      ||||||||||||||||  |||||||  | || |  || || ||
Db  20610 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 20669

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          ||||||        ||| |  ||| ||   |   ||||||||  ||  ||
Db  20670 GTTCCGCAGTGACCTGTCGCGGCTCCTGACGAAGCTGGGCTGTACCGGCC 20719


RESULT 13
US-10-251-385-65
; Sequence 65, Application US/10251385
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 65
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-65

Query Match 12.7%; Score 238.4; DB 11; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2.1e-41;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

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Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    144 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 203

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    204 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 263

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    264 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 323

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    324 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 383

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    384 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 443

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    444 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 503

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    504 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 563

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
Db    564 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 623

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    624 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 683

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db    684 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 743

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db    744 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 803

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db    804 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 863

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
Db    864 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 923

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
Db    924 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 983

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
Db    984 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1033
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RESULT 14
US-10-251-385-199

; Sequence 199, Application US/10251385
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 199
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-199

Query Match 12.7%; Score 238.4; DB 11; Length 1119;
Best Local Similarity 56.9%; Pred. No. 2.1e-41;
Matches 506; Conservative 0; Mismatches 366; Indels 18; Gaps 3;

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Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
Db    144 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 203

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
Db    204 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 263

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
Db    264 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 323

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
Db    324 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 383

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
Db    384 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 443

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
Db    444 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 503

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
Db    504 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 563

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC------------CACCCACTGCCAATACAA 930
Db    564 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 623

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
Db    624 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 683

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
Db    684 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 743

Qy   1045 TTCCAGGGGCCAGCGGCGCCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
Db    744 CCAGCGGCGCCCTCAGCGGCAGAAGGCAAAAAGGGTGGCCATCCTGGTGACAAGCATCTT 803

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
Db    804 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 863
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Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
          ||  ||| |   | |||    |   |  ||    |   ||||||||   | |
Db    864 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 923

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
            |||||||      ||||||||||||||||||  |||||||  | || |  || || ||
Db    924 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 983

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          |||||||        ||| |  ||| ||       ||||||||  ||  ||
Db    984 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1033


RESULT 15
US-09-442-384B-424
; Sequence 424, Application US/09442384B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT:  Lukashev, Matvey
;  TITLE OF INVENTION: Hematology/Immunology Array
;  FILE REFERENCE: CLON-006CIP15
;  CURRENT APPLICATION NUMBER: US/09/442,384B
;  CURRENT FILING DATE:  1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 830
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 424
;   LENGTH: 2818
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-442-384B-424

  Query Match            12.7%;  Score 238.4;  DB 9;  Length 2818;
  Best Local Similarity  56.9%;  Pred. No. 2.5e-41;
  Matches  506;  Conservative    0;  Mismatches  366;  Indels   18;  Gaps    3;

Qy    463 CTTCGACCGGGCCTTCCTGCCAGCCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGG 522
          |||| |    |  ||| |||| |    ||||||||||| |||| || |||||  || | ||
Db    228 CTTCAAGGCCGTGTTCGTGCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGG 287

Qy    523 CAACGGCGCGGTGGCAGCCGTGCTGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACAC 582
          ||||| |  ||||   |   | |||  | | |  |||    | |  ||   ||| || ||
Db    288 CAACGTCCTGGTGCTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGAC 347

Qy    583 CTTCCTGCTCCACCTAGCTGTAGCAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGC 642
          ||||||| ||||||| || || || |||   ||||||||  | |   ||||  |    |
Db    348 CTTCCTGTTCCACCTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGT 407

Qy    643 AGTGGACGCTGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCT 702
            |  || |   | ||    |||||| | ||  |   ||||||||||    |    ||||||
Db    408 GGCCGAGGGCTCTGTGGGCTGGGTCCTGGGGACCTTCCTCTGCAAAACTGTGATTGCCCT 467

Qy    703 CTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTA 762
             |||  ||||||||||||    |   ||| || ||||||||||||  | | ||||||||
Db    468 GCACAAAGTCAACTTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTA 527

Qy    763 CCTGAACATAGTTCATGCCACCCAGCTCTACCGCCGGGGGCCCCCGGCCCGCGTGACCCT 822
          ||||  ||| || || |||  |||   ||||||||   | | ||    |  | |   | |
Db    528 CCTGGCCATTGTCCACGCCGTCCATGCCTACCGCCACCGCCGCCTCCTCTCCATCCACAT 587

Qy    823 CACCTGCCTGGCTGTCTGGGGGCTCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCT 882
          ||||||   | |  ||||| | |  || | ||  | ||| | |||||  |  |||||
Db    588 CACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTTGCCTTGCCAGAGATTCTCTTCGC 647

Qy    883 GTCGGCCCACCACGACGAGCGCCTCAACGC-----------CACCCACTGCCAATACAA 930
            | |  ||| | | | | |  |||| |            ||||  || |||| | ||
Db    648 CAAAGTCAGCCAAGGCCATCACAACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAA 707

Qy    931 CTTCCCACA---GGTGGGCCGCACGGCTCTGCGGGTGCTGCAGCTGGTGGCTGGCTTTCT 987
          |    || |   |   | | |      |    ||  | ||  | |  ||||| || || ||
Db    708 CCAAGCAGAAACGCATGCCTGGTTCACCTCCCGATTCCTCTACCATGTGGCGGGATTCCT 767

Qy    988 GCTGCCCCTGCTGGTCATGGCCTACTGCTATGCCCACATCCTGGCCGTGCTG---CTGGT 1044
          ||||||| ||||||| |||| ||  ||||| |       |  ||  |  | ||   | ||
Db    768 GCTGCCCATGCTGGTGATGGGCTGGTGCTACGTGGGGGTAGTGCACAGGTTGCGCCAGGC 827

Qy   1045 TTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTCGTGGTGGCCTT 1104
            || |||  | ||| | |  |||  |  || |||    |  ||||         |||
Db    828 CCAGCGGCGCCCTCAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTT 887

Qy   1105 TGCCCTCTGCTGGACCCCCTATCACCTGGTGGTGCTGGTGGACATCCTCATGGACCTGGG 1164
            |||||||||| | ||||| ||| | ||  |  |  ||||||  |||   |   |||
Db    888 CTTCCTCTGCTGGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAA 947

Qy   1165 CGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTC 1224
          ||  ||| |   | |||    |   |  ||    |   ||||||||   | |
Db    948 GGCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGA 1007

Qy   1225 AGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCTATGCCTTTGTAGGGGTCAA 1284
            |||||||      ||||||||||||||||||  |||||||  | || |  || || ||
Db   1008 GTTCCTGGGCCTGGCCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAA 1067

Qy   1285 GTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCTGCCCCAACC 1334
          |||||||        ||| |  ||| ||       ||||||||  ||  ||
Db   1068 GTTCCGCAGTGACCTGTCGCGGCTCCTGACCAAGCTGGGCTGTACCGGCC 1117


Search completed: November  2, 2002, 04:32:28
Job time : 507 secs
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